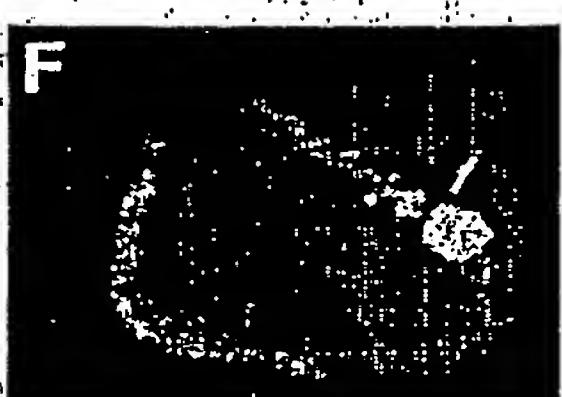
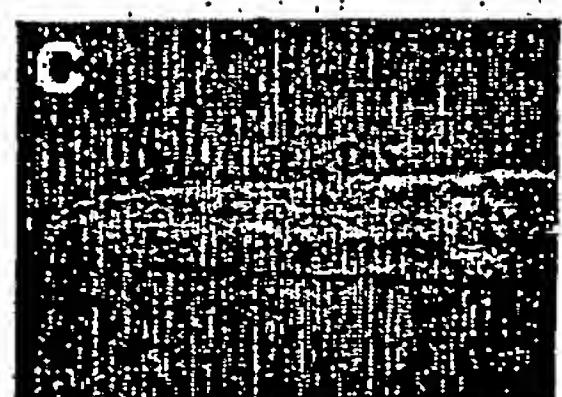


Fig. 1A-1C

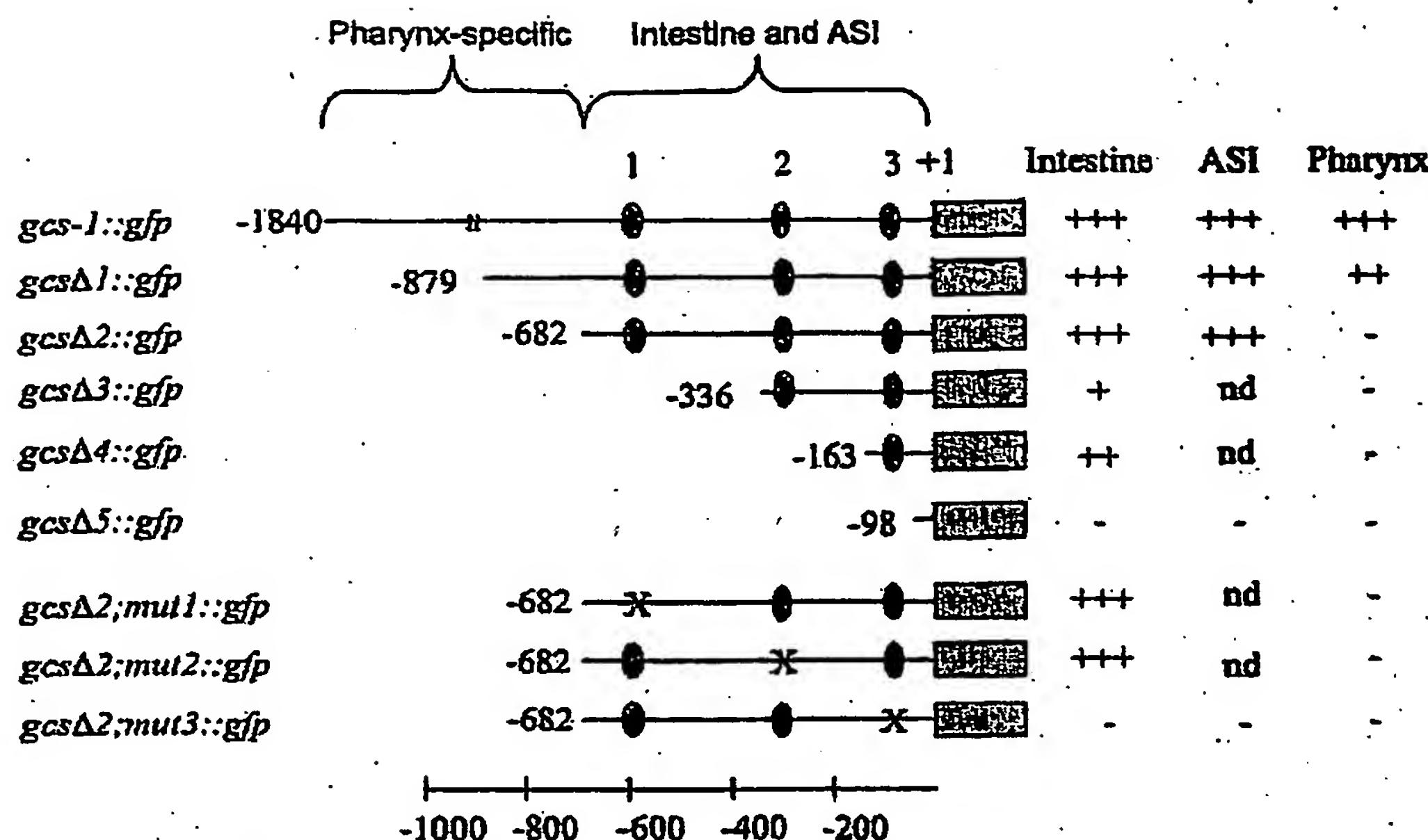
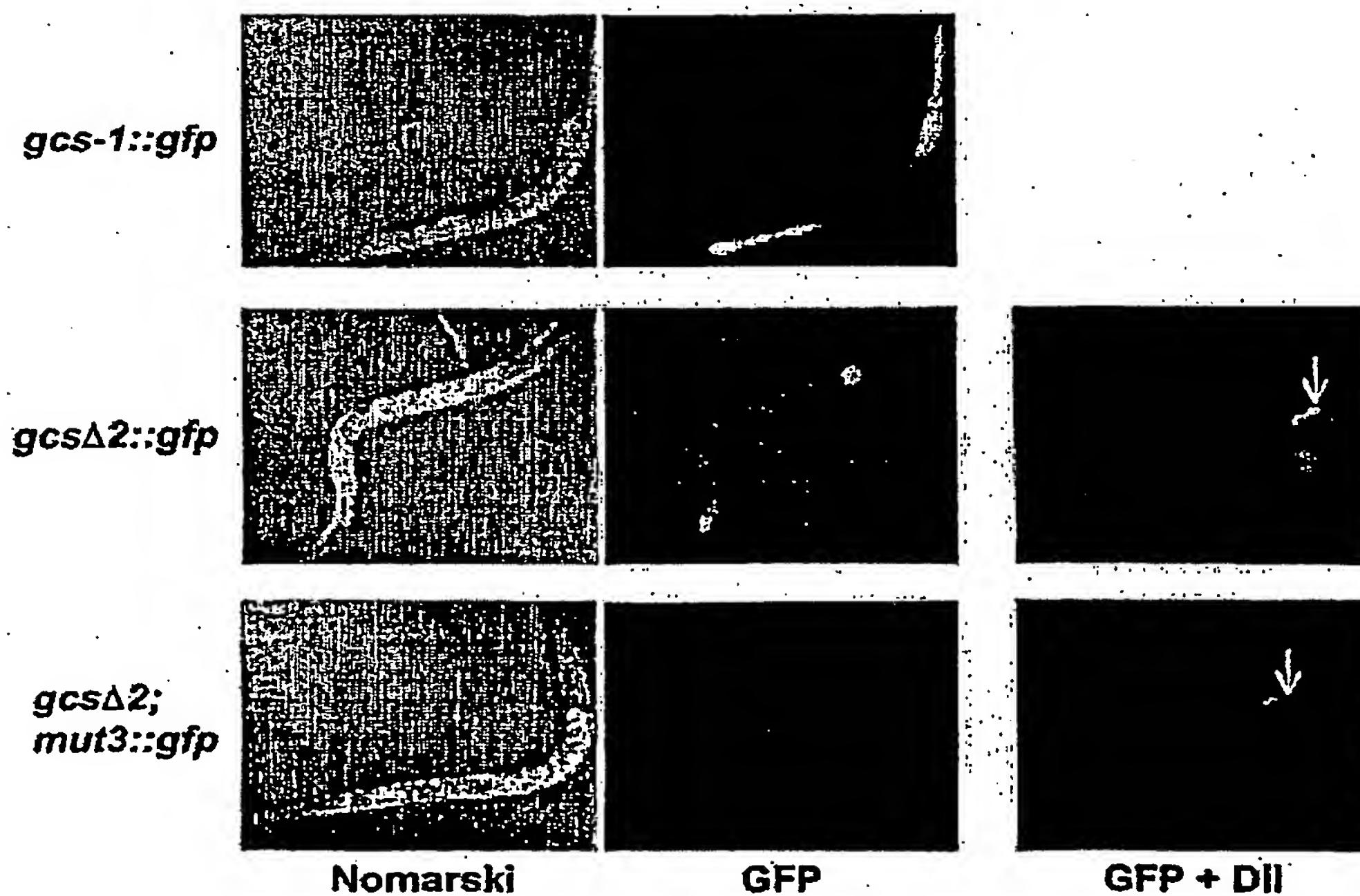
*skn-1(+)*



*skn-1(zu67)*



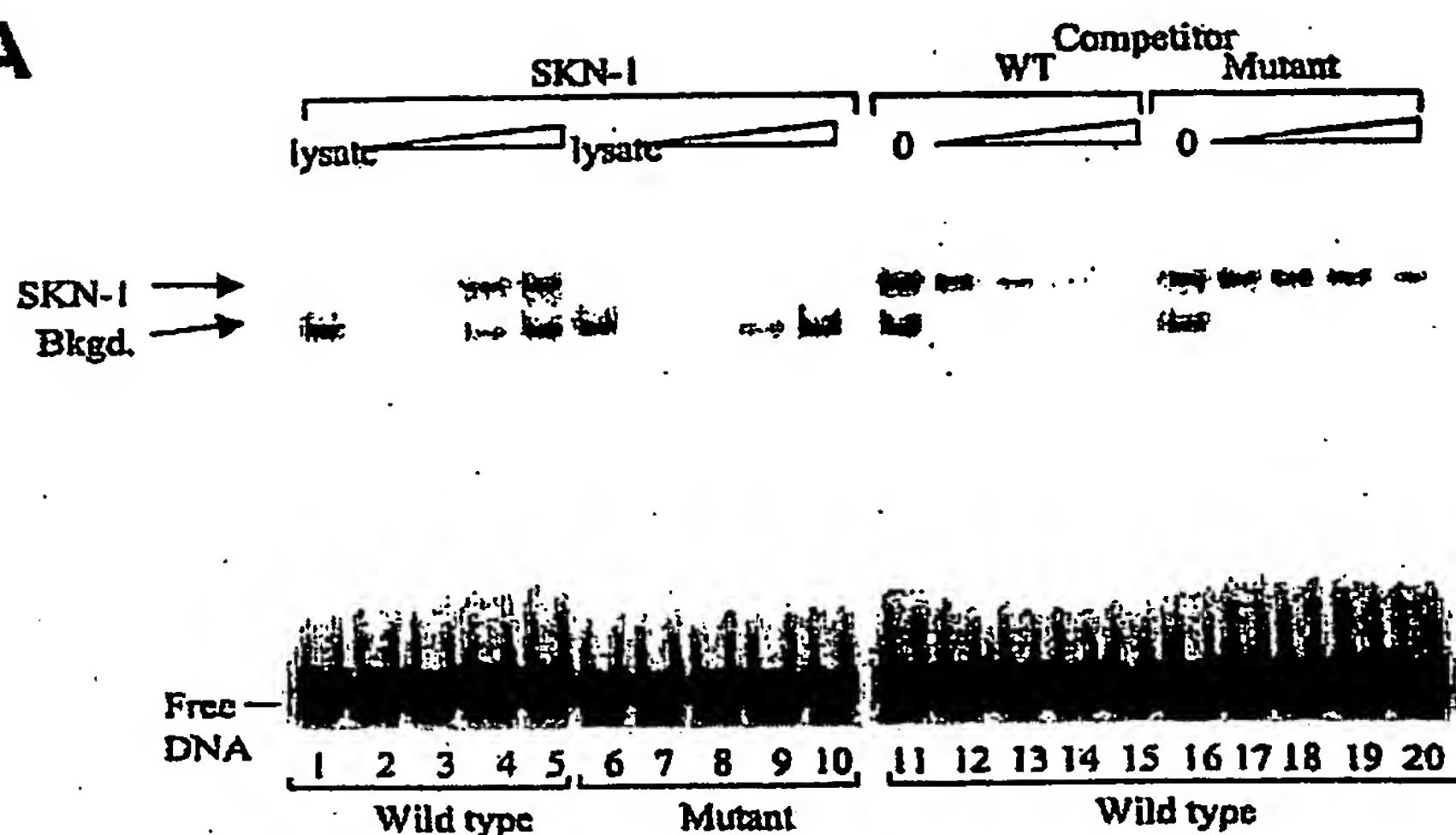
Fig. 2A-2L

**A****B****C**

<i>gcs-1</i> -124	CA-CTTATCATCATGA-GATTAAATGTTGTTGTTTAT-TTTCTT-83
<i>med-1</i> -127	CACCTCTGTCATCATGATGATTTTGGAG-CATTATCATCATTTCTT-83
<i>med-2</i> -127	CACCTCTGTCATCATGATGATTTTAGAG-CATTATCATCATTTCTT-83

Fig. 3A-3C

**A**



**B**

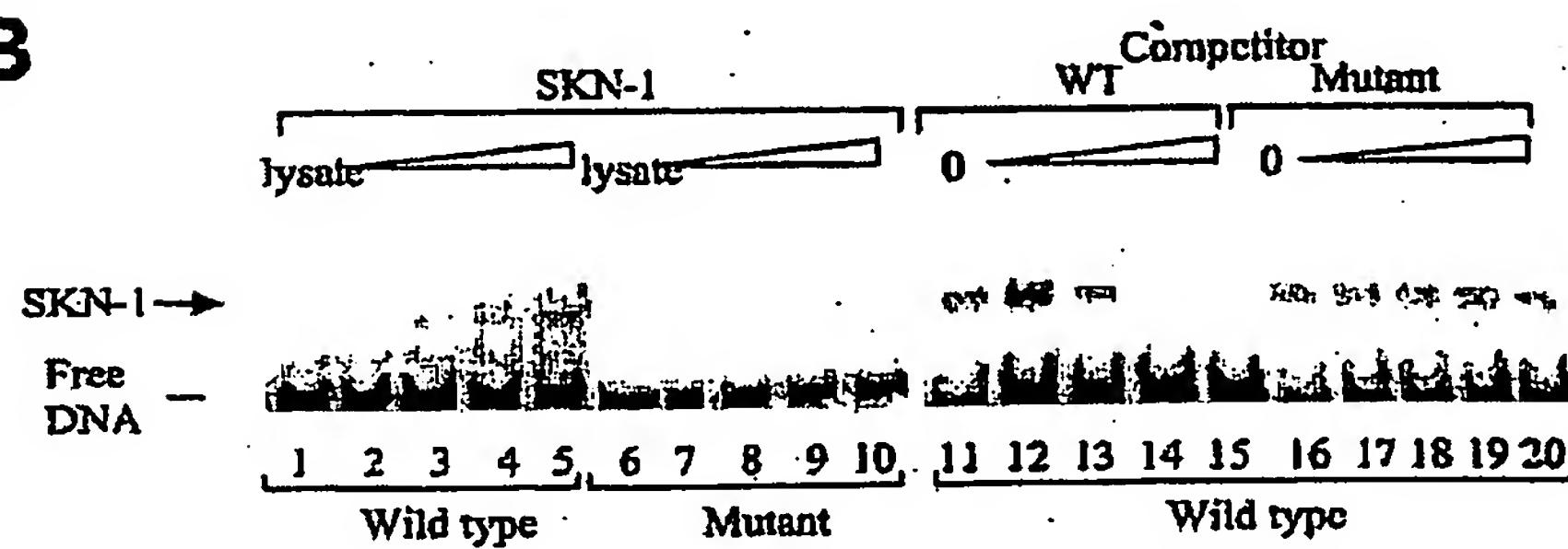


Fig. 4A-4B

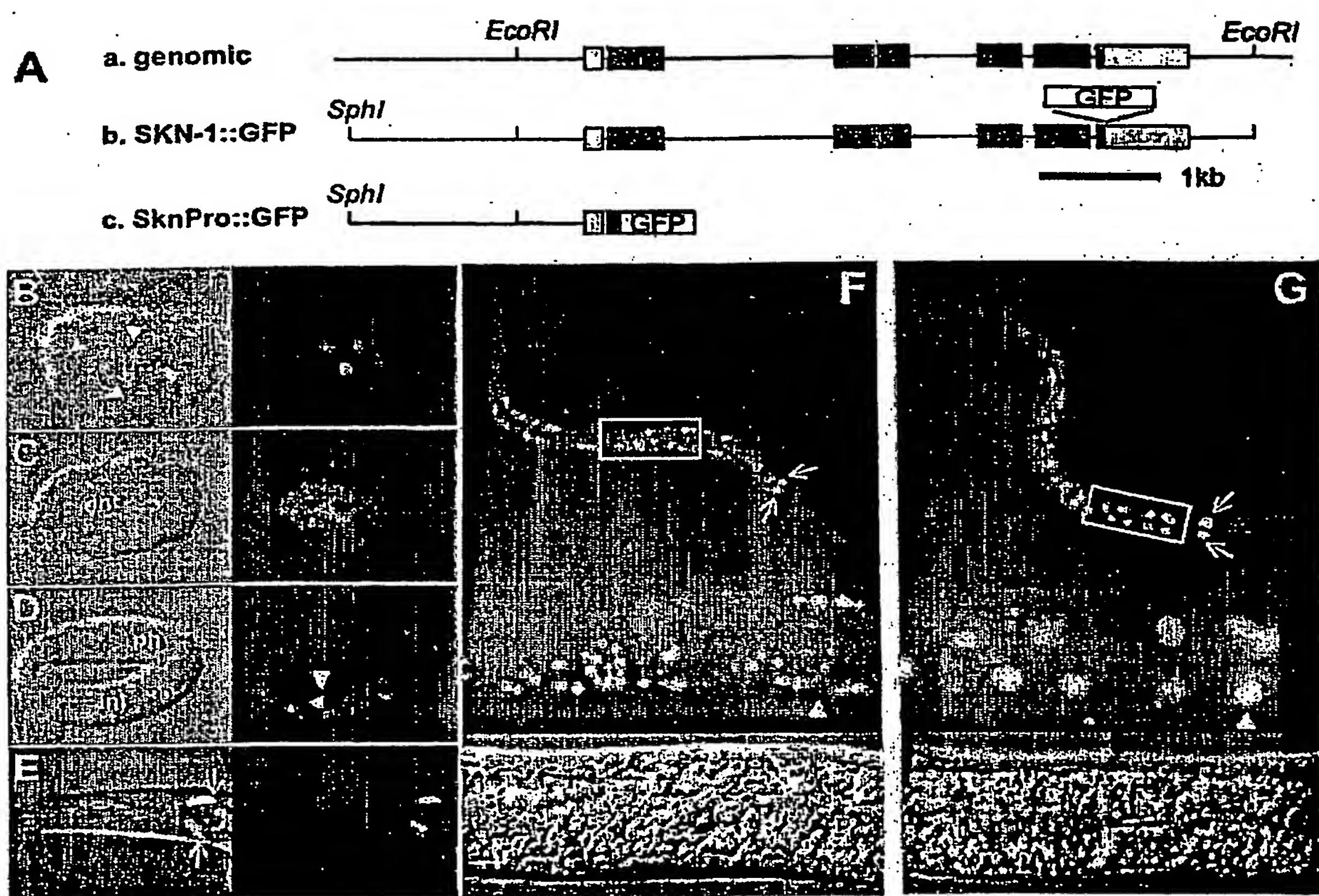


Fig. 5A-5G

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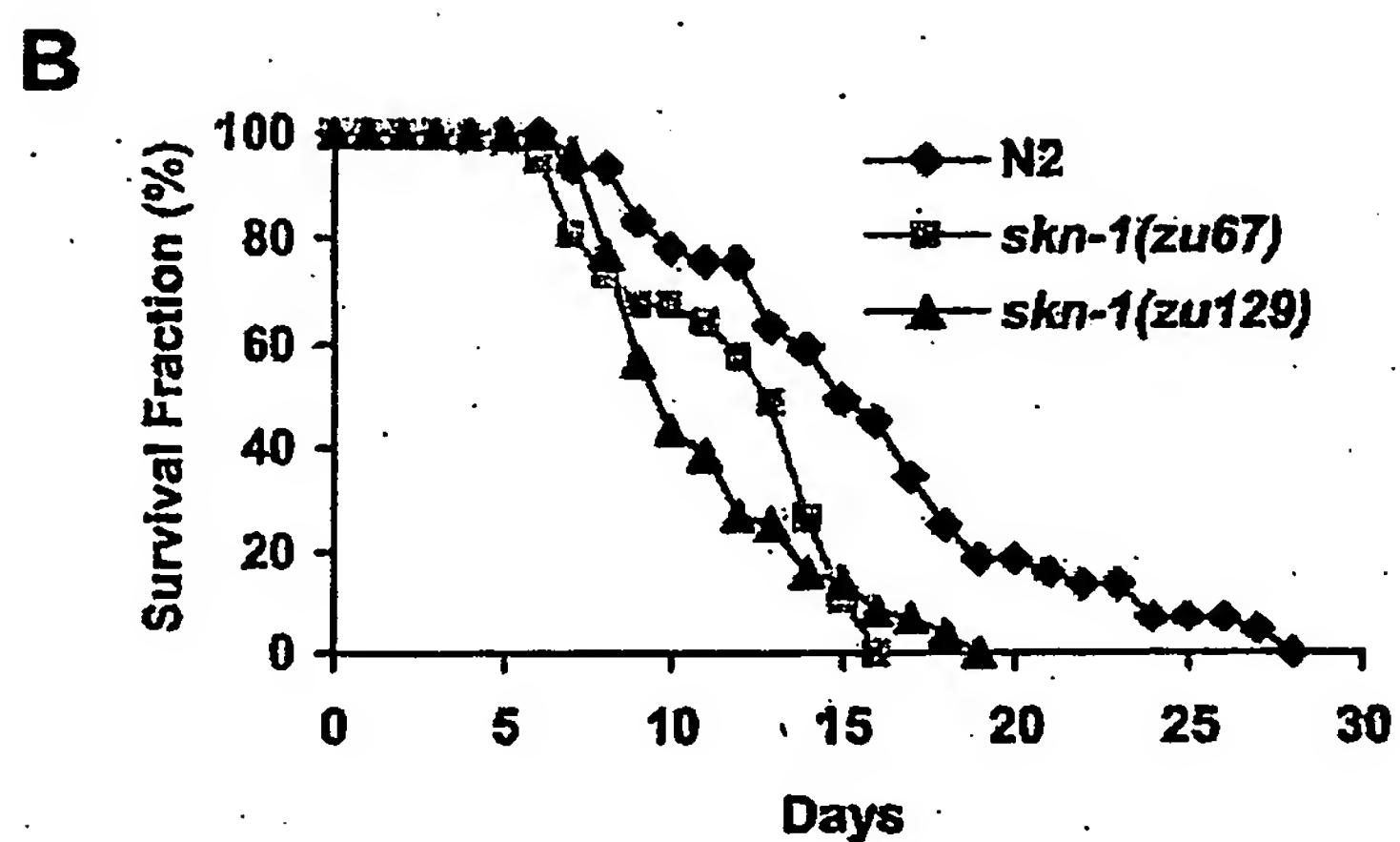
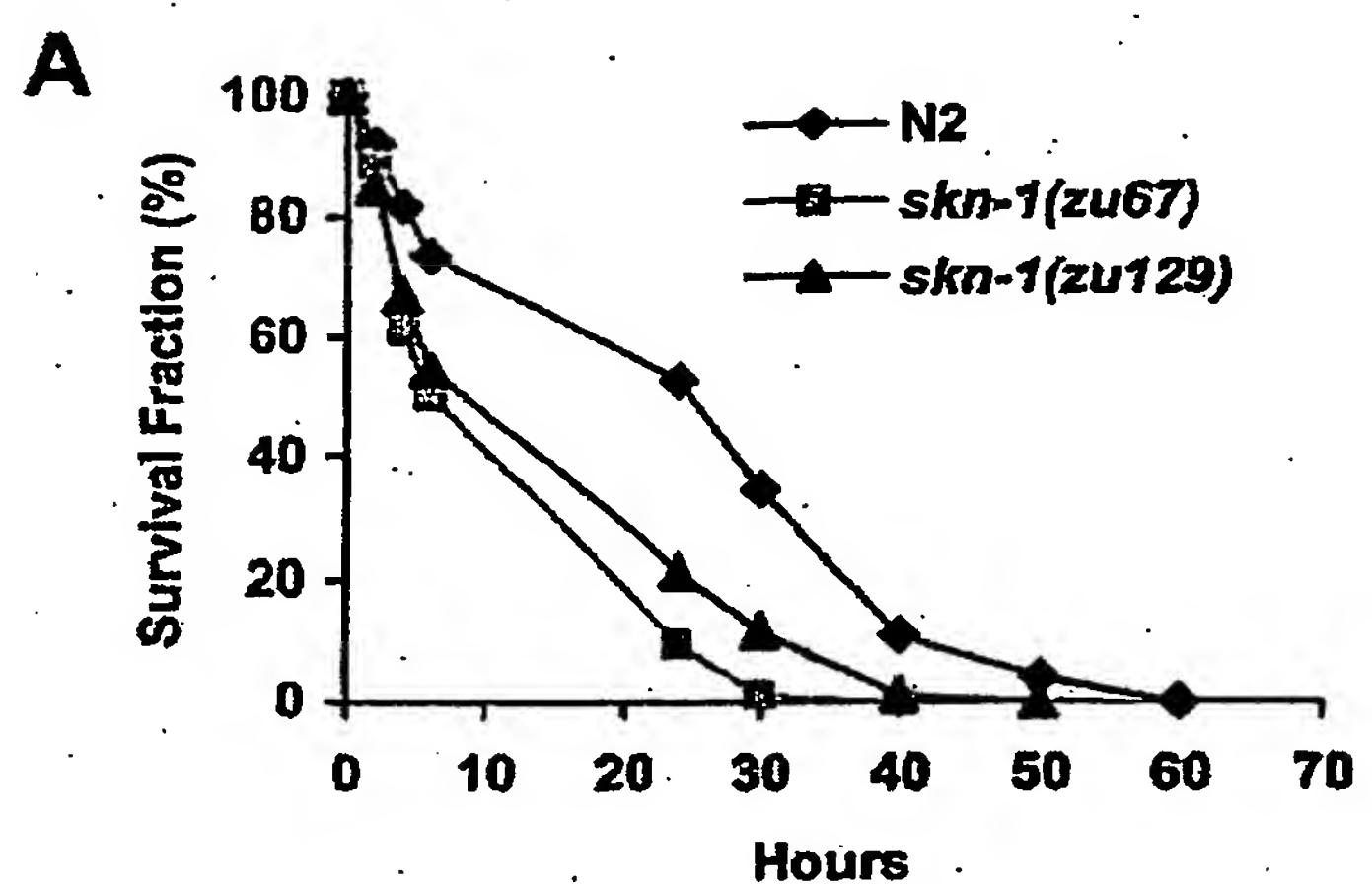
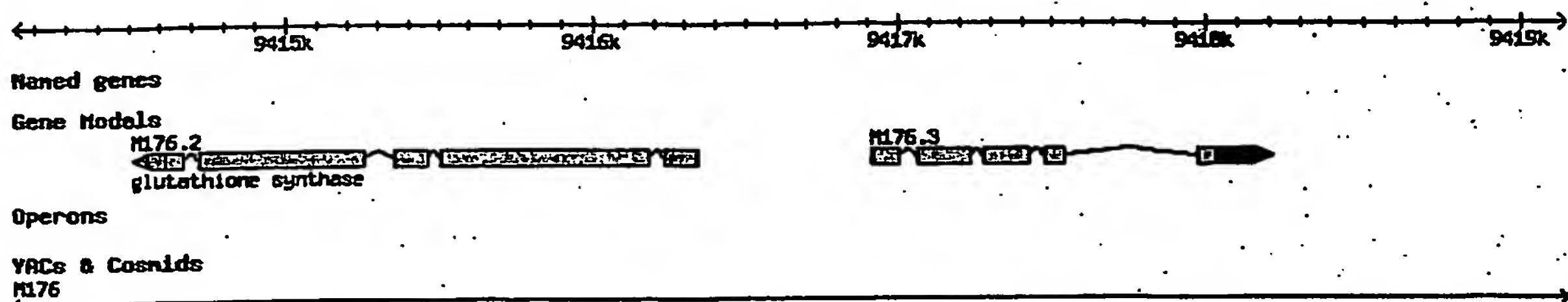


Fig. 6A-6B



The M176.2 gene is located on chromosome II. Regulatory sequences can be found e.g., in the region between 9416340 and 9415915. An exemplary sequence of this region is as follows:

GACAATTATCGATTAATAAAAGTTAACAGACACGAGAAATTAAATATAAAAAATTGAATTGTTTATTT  
 GTTGTGTTGTGTAGAAAAATAATTTGATAGAAACAAAAATTAGCGTAAATAAATAGCTAGCGCAA  
 TACTCGTGCACGAGATGTGCCAGCAGCTCCTGACGCAAAACGTGACGTTAGCACCAAAATGATT  
 -378  
 TGCTCTTGAGTTCTTGTGTTGGAGCAAATTTCATGCCAATCCCTTCTTTCAAATTTCCTG  
 TTAAATTCAATGTAATAACTATTATTCAATGTCAATTACAACAAATAAGCATCCAAGATTTCATAAACT  
 -243  
 CGTTCAAACCTCCTTACCACTCGAAAAGCAATATCTCCGACTCCTCAAAGAGAAATGATGACAAA  
 -169  
 CATAGAAACCTCACGTTACGTTGTCATCACGATTCAGTGCTCACTTTCTCATTCTCGCT  
 -137  
 TAATTCATTTGTCACTCTCGCGTCATGTTGCATTTGAAAGCATTATTAAAAGTGA  
 TAATTCGTAATTTCAAGAATGGCT

FIG. 7

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Exemplary M176.1 sequences:

**Amino Acid Sequence**

MAQKDDRILL LNAPRLPLED DKLNELTADL HDWAHANGLV MRLSTDKLSS EVCQTTPLTL LPSPFPKNVF EEAVHIQNLF ASLYHFIAYE FDFLIDIHKN VVKTDDFTRN MVEILKKVKA QGLKQPVTLA IQRSQDMCHK DQYSAEYGLK QIEINNIASS MGAHALRLTE WHIRVLKALN ISDDVIQRAI PENKPIPMIA EALFKAWSHF SNPAAVVLVV VENVNQNQID QRHVEYELEK LGVPMTCIIR RNLTQCYEQL SLNDRSDLMI DGRQVAIVYF RAGYSPDHYP STKEWEARER MELSTAIKTP WIGLQVANTK KTQQVLSEDG VLERFIGKPR EARDIRASFA GMWALENTDE VTMKVVAGAQ KHPEAFVLKP QTEGGAALHT GDEMVQMLRE LPEEERGAFI LMEKLKPMII ENYLVLAKKP ITFAKAVSEL GVYGYAFGRK DAPELKTAGH LLRTKPESTA MGGVAAGHAV VDTPFLYEFI

**Spliced mRNA**

aaagaATGGCT CAAAAAGATG ACCGGATTG GCTGTTGAAT GCTCCAAGGC TCCCCTCGA AGATGATAAG CTCAACGAGC TCACCGCTGA TCTTCACGAT TGGGCTCATG CTAATGGCT TGTCATCGT CTATCAACCG ACAAGTTGAG CAGCGAAGTT TGTCAAACCA CTCCATTAAAC ACTTCTTCCA TCTCCATTCC CGAAAAATGT TTTGAAGAA GCAGTTCATATA TTCAAGAACCT TTTCGCAAGT CTTTATCACT TCATAGCTTA TGAATTGAT TTTCTAATCG ATATTCTAA AAATGTCGTG AAAACTGATG ATTTCACACG GAATATGGTT GAGATCTGA AGAAAGTCAA AGCCCAAGGA CTCAAGCAAC CAGTCACCT CGCGATTCAA CGATCTGATT ATATGTGTCA TAAGGATCAA TATTCAAGCGG AATATGGACT GAAACAAATT GAAATAAAACA ATATGCCCTC GTCAATGGGA GCACATGCTC TACGGCTCAC CGAATGGCAT ATCAGAGTTC TTAAAGCGTT GAACATTTCC GATGACGTCA TTCAAAGAGC AAATTCCAGAA AACAAAGCCAA TTCCAATGAT CGCTGAAGCT TTATTCAAGG CCTGGTCCCCTTTTCAAC CCAGCAGCTG TGGTTCTGT CGTTGTAGAA AACGTCAATC AAAATCAGAT TGATCAACGC CACGTGGAAT ATGAACCTGA AAAGTTAGGA GTACCGATGA CATGTATTAT TAGAAGAAAT TTAACACAAT GCTATGAACA ATTATCATTG AATGATAGAA GCGATTGAT GATTGATGGG CGTCAAGTAG CAATTGTTA CTTCAAGAGCA GGATACTCAC CTGATCATTA TCCATCTACA AAAGAATGGG AAGCACGTGA GCGTATGGAA CTTTCCACCG CTATCAAAC TCCATGGATC GGGCTACAGG TGGCAAATAC TAAGAAGACC CAGCAGGTTT TTTCTGAAGA TGGAGTACTC GAAAGATTCA TCGGAAAACC ACGAGAAGCT CGCGATATTG GAGCTTCATT CGCAGGAATG TGGGCTTGG AGAACACTGA TGAAGTGAAT ATGAAAGTCG TGGCTGGAGC TCAAAAACAT CCAGAAGCGT TTGTTCTGAA GCCACAAACT GAAGGTGGAG CCGCATTGCA CACCGGTGAT GAGATGGTTC AAATGCTCCG AGAACTTCCG GAAGAAGAGC GTGGAGCTT CATTGGATG GAGAAACTGA AACCGATGAT TATTGAAAAC TACCTGGTTC TTGCAAAGAA GCCGATCACA TTTGCTAAGG CTGTTAGTGA ACTTGGAGTG TATGGTTATG CATTGGAAAG GAAGGATGCA CCTGAGCTTA AGACTGCTGG GCATTTGCTC CGAACGAAAC CGGAATCCAC AGCTATGGGT GGAGTAGCCG CCGGACATGC TGTTGTCGAC ACCCCATTCC TCTACGAATT TATTGATT cgaacataat cagaaaactc aacaaaaatg ctgtgatatg aaaccatgg ctatggat cttttgtgt ttgtaaattt aatcattgta atttattgaa tgt

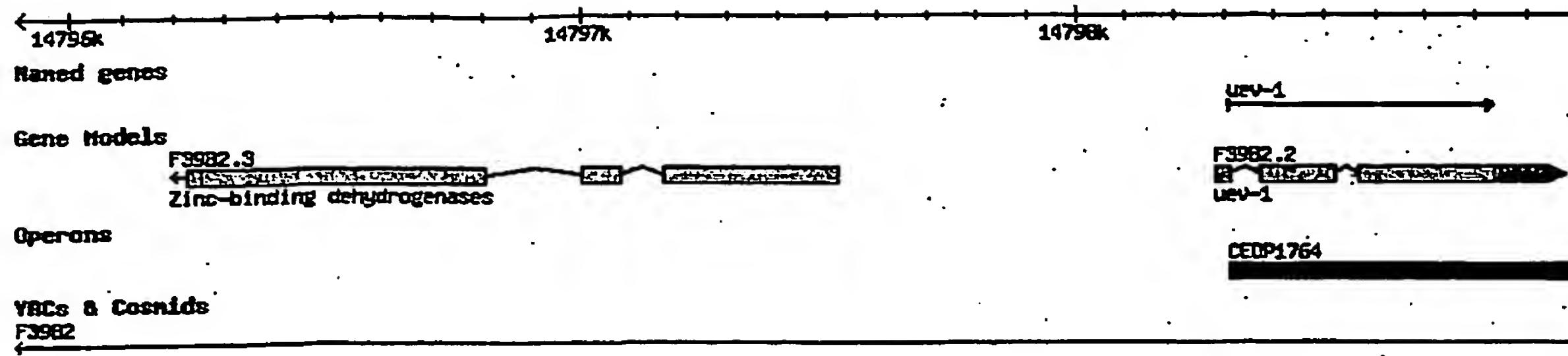
**FIG. 8**

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The F39B2.3 gene is located on chromosome I. Regulatory sequences can be found e.g., in the region between 14 797 521 and 14 798 310. An exemplary sequence of this region is as follows:

CATTTGAAAGTGCCAAGTTGCTGGAACGCTGAAAATTGAAATTATTAACAAAGAAATTGCTTTAAAA  
TCCGAAAAATCAAGAAAAATCGATAATTCGTCGGACAATCCGCCTGCTAGCACGGCTTGACGCTCGTT  
TGCGCGCGCTCATTGATTGTGAGTGCCAGTGGAGCGCGTTGCTAAGGCTAACTGTGTAGTCCT  
CTCGGACAAGATCTGTGAACATTGAAATGAAACACTGGGTTCAATAAAATCACAGAAAATGATGACAA  
-518  
TTTGTTGCGACCGAAAAAAATTATAAAATTGAATATTGGTTATCATCGTTCAATTTGTTGT  
-469  
ATTAAAGGCACAGCTGCTAAAATTGTTTTTTCAATTGCTAAAAGAAAATCAATTCTGAT  
TTTTGTTGAGTTCCCGTGCATCAATGTCCTAGCTTTAAAATTGTTTTGTTATGTAATTCTAAT  
CAAATTGTCGAATTCAGAGATTTCTGCTAAAACACTAAAATAGTCTAAAGTCGATAATTGAT  
AAACATTACTCAAACCTTTACGGAAAATGAAACAAAGTTGCAAAATATAGTAATTGCAATT  
CTGAACGCGTACTAAAGGTACACGGTTGATTGGATGGTCCGCCACAAAGTGTACCGATAACATT  
TTCTCGCTGCGAGACCCATCCGAATAATCCGTGCGCCTAATCAGTGCAGTACGCATTCAATTACTG  
ATAAGTGCCATTAGAACAAATG

**FIG. 9**

Exemplary F39B2.3 sequences:

Amino Acid Sequence

MSKSICKSSM RAAVVRFFGA PDVIEAVESD MPRLEKNQVL VRNYAAGVNP VDTYIRAGQY GKLPNLPYVP GKDGAGFVEL  
VGESVKNVKV GDRVWYGYSEA DSTAEYVAVN RPFLPEGVS FEEGASLGVP YLTAYRALFH LAGAKTGDVI LVHGASGGVG  
SALMQLAAWR NIEAVGTTAGS ADGIRFVKSL GARNVYNHSD KQYVSKMKND YPGGFNHIFE MAAHTNLNTD LGLLAPRGRV  
AVIGNRAETT INARQLMVTE GAVYGVVALGM SSEAELLDFG INIVSFLKET EFRPLINKLY RLEQLGLARE EIMNNKGAKG  
NLVVQIEH

Spliced mRNA

ATGAGCAAAT CGATTTGCAA ATCAAGCATG CGCGCAGCTG TAGTCCGACG ATTCGGAGCA CCTGATGTCA TAGAAGCCGT  
CGAGAGTGAT ATGCCCAAGGC TTGAAAAAAA CCAGGTTCTC GTTCGGAATT ACGCTGCCGG TGTCAATCCA GTTGACACAT  
ATATTCGTGC TGGTCAGTAT GGAAAACATAC CAAATCTCC ATATGTACCA GGAAAAGATG GAGCCGGATT CGTCGAACCT  
GTGGGAGAAA GCGTTAAAAA TGTGAAAGTC GGCAGATCGAG TCTGGTATGG ATCAGAAGCG GACAGTACAG CAGAGTATGT  
TGCAGGTGAAT CGACCATTG AGTTGCCGGA AGGAGTTCG TTTGAGGAAG GAGCTTCTCT CGGAGTGCCT TATCTTACCG  
CTTATCGTGC ATTGTTTCAT CTTGCTGGT CAAAGACTGG CGACGTTATA CTTGTACACG GAGCATCTGG TGGAGTGGGA  
AGTGCAGTGA TGCAGCTGGC TGCCTGGAGG AACATTGAAG CTGTTGGCAC TGCTGGATCT GCTGATGGGA TCCGGTTCGT  
GAAGAGTCTT GGTGCACCGA ATGTCTATAA TCATTGCGAT AAGCAATATG TGTGAAAAT GAAAAATGAT TATCCAGGAG  
GCTTCAACCA CATTTCGAA ATGGCTGCTC ACACAAATCT GAACACGGAC CTCGGATTGC TGGCTCCACG TGGTAGAGTT  
GCAGTAATTG GAAATCGCGC CGAGACCACG ATCAACGCAA GACAACATTAT GGTTACAGAA GGAGCTGTTT ACGGTGTAGC  
ATTGGGAATG TCTTCCGAGG CTGAGCTCTT GGACTTTGGC ATCAACATTG TCTCATTCTT GAAGGAAACC GAGTTTGTGTC  
CACTTATAAA CAAATTGTAT CGTCTCGAGC AATTAGGACT GGCTCATGAG GAAATTATGA ACAACAAAGGG AGCGAAAGGA  
AATCTTGTAG TGCAAATCGA ACATTAATTc attatttaa cacgccattt aaaggaa

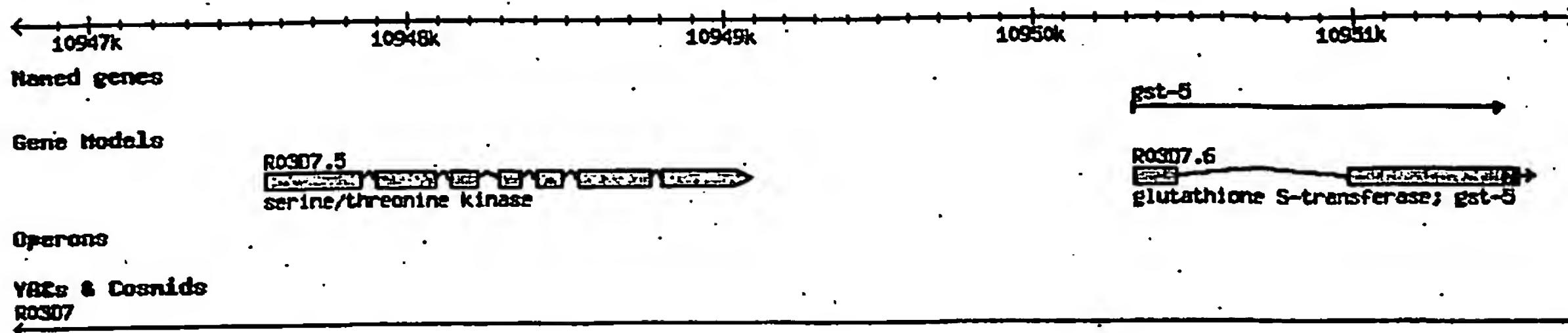
FIG. 10

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The R03D7.6 gene is located on chromosome II. Regulatory sequences can be found e.g., in the region between 10949088 and 10950317. An exemplary sequence of this region is as follows :

AGAACTTTCGAGAAGTCTACCGTTAGTTTCGAAATAGTAATTTAGTAGTGACGTTATAAAGGTTACATGATTT  
GGTTTGAAATTTTAGGAGTTATTCTATAAAAACAAAGTAACCATGGACATTCCAGAAGTCTATAGTACACGCGATCC  
TACCGTACCCCTCAGTATTCTATCAGATTGATAGCTTCGGTAGTCAGGTACAGCCTAAAAAATTCTGCTTGCCTTT  
TGCCTACATGTCTGCCTACCTCAGTCATAATGCCTACATAATG

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ATTTTTCCAATTGAAACTTGCAGACAGAAATTCAAATGGCAAAAGAAACAAACACCGAAACATTAAATCA

CATTCTTTCATATCAGTTCTGTCAAAGCACATTCTGGAGTCTGTGTATTTCGTCTTATGTGATCGG  
TGTTGTGAAATTGATGTTGATAACATACTTTTGAAACAAAAAGTGAATTGATTAGGCTTGAATTGAGA  
TATGTTCGTGTGATACTTTGCGATTCTCGAGCAAAACACGGTATCCGGTCTCGACACGACA  
GCTGATGTGCGCCTTGAAAGAGTACTGTAATTCAACCTTCGTTGCGGAATTTCATAGTTCTCGTTCAAAATAT  
ATGTATTATTAAACAAAAACTAAAACAAATTGAGAACACATAAATTGTGAAAATCAATGAGACCACAGCAAA  
AATTGTATCTACAGTACTCTTAAAGGCGCACATCCGTTATTTCAGCAAAATGTCGCTTCGAGACCGGGTACC  
GTATTTTTGTGCAAAACTTAGGTCTAGGTAAATTAAAAAAATTCCACAAAATAGAATCTAGAGCTTCCAT  
TAAATTTTGATGACATTGAAAATTCATGATGATTTCACAAATTGAAATATCCCTTTCACCTGGTCC

-302

-282

ACTGAATTCTCTTCCGAAAGACCACACAATTTCAGGGCTCCGCCATTCTGGTTGTAGCCTCCGACCTACGT  
TTTGATGACAATTGTGAGAGAAGTGAAGAGGTTCAGACACAAAAGCGACGTGGTCGAATGA

-149

GTATAAATAGAGAGTGAAGTTCCAATTCCCTACAATTGTTGCAATCCACTTCAAAAAACACAACCTCAA  
TCAAAAATCATTATGGTT

**FIG. 11**

Exemplary R03D7.6 (gst-5) sequences:

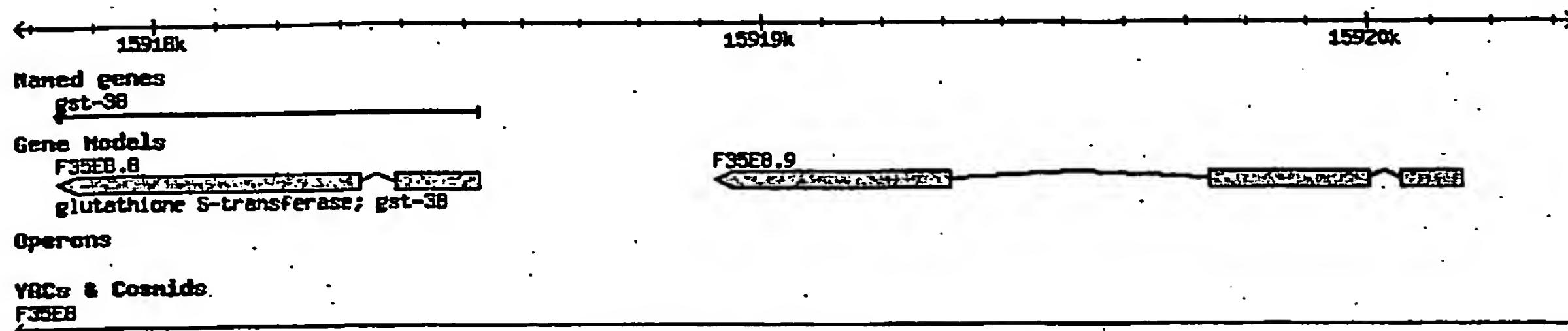
**Amino Acid Sequence**

MVSYKLTYFN GRGAGEVSRQ IFAYAGQQYE DNRVTQEWP ALKETCAAFF GQLPFLEVVG KKLAQSHAIA RFLAREFKLN  
GKTAWEEAQV NSLADQYKDY SSEARPYFYA VMGFPGDVE TLKKDIFLPA FEKFYGFVN FLKASGSGFL VGDSLTWIDL  
AIAQHSADLI AKGGDFSKFP ELKAHAEKIQ AIPQIKKWIE TRPVTPF

**Spliced mRNA**

ATGGTTTCCT ACAAGTTGAC CTACTTCAAT GGACGTGGCG CTGGAGAAGT GTCTCGTCAG ATTTTCGCCT ATGCCGGACA  
ACAATACGAG GATAATAGAG TCACTCAGGA ACAATGGCCA GCATTGAAAG AAACCTGCGC TGCTCCATTG GGACAACTTC  
CATTCCCTCGA AGTCGACGGT AAGAAGCTTG CTCAATCCCA CGCGATTGCT CGTTTCTTGG CTCGTGAGTT CAAGCTCAAC  
GGAAAAACCG CCTGGGAAGA GGCTCAAGTG AACTCTCTTG CCGATCAATA CAAGGATTAT TCAAGTGAGG CTCGTCCATA  
TTTCTACGCT GTCATGGGAT TCGGTCCAGG AGACGTTGAA ACTTTGAAGA AAGACATCTT CCTTCCAGCA TTTGAAAAGT  
TCTACGGATT CTTGGTCAAC TTCTTGAAGG CTTCGGGATC CGGATTCCCT GTCGGAGACT CTTTGACCTG GATTGACTTG  
GCTATTGCCA AACATTCAAGC TGATTGATT GCCAAGGGAG GTGATTTCAG CAAGTTCCA GAGCTCAAGG CTCATGCCGA  
GAAGATCCAG GCGATTCCAC AAATCAAGAA ATGGATCGAG ACCCGTCCAG TCACACCATT CTAAatagct gtataaaatc  
tgcaaataaa tattttttt tttt

**FIG. 12**



The F35E8.8 gene is located on chromosome V. Regulatory sequences can be found e.g., in the region between 15 917 841 and 15 918 925. An exemplary sequence from in or around this region is as follows:

TCTCATTCTCTCAAGACATAACACACGGGCTGACGACCATATCATCAACGACGATTTTAGGAAC TG  
TACTTTATCTGTGTCTGACCAACACGTGTGAATGAAGTTCACTGGAAAATTGTTGAAACACTGCAA  
AGAATTTCGAATTGGATGATAATTAAATGCCATTATCAGTTAATACGCCACTCTAGTCTTGATT  
-240

CTTTGCACACACACACACACACACACACACACACTCACAAACACGCCCTGAAATTGCAATATG  
CTGATTTAACGAGAAAACATTGATGACAATAACTGGCGTATTAATATAAGGGAAAATTCAATTCA  
-94

GATTCTCAACGGTTATTTCTGTACAACCTTCCTAATATTACCCATGGTTT

**FIG. 13**

Exemplary F35E8.8 (gst-38) sequences:

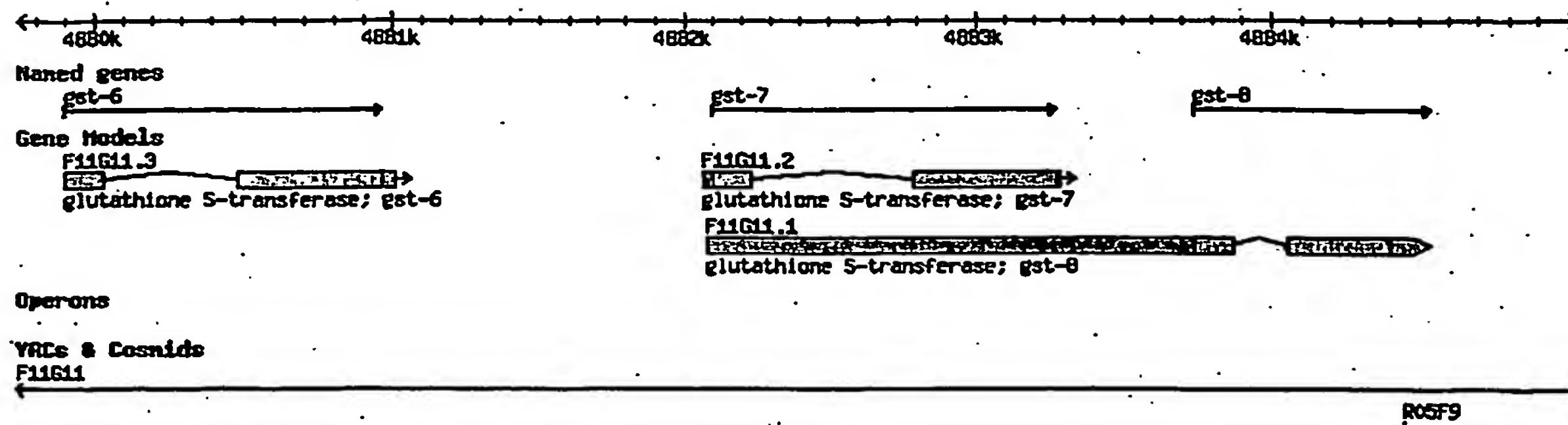
**Amino Acid Sequence**

MVSYKLTYFD GRGAGELCRQ IFAAAEQKYE DNRLTDEEWE KFKAAGKTPY NQLPMLEVDG KPLAQSHAMA RYLAREFGFN  
GKSRRWEAQV NSLADQYKDY YAEARPYLAV KLGYTEGDAE ALYTSVYLPV FKKHYGFFVN ALKASGSGFL VGNSLTFIDL  
LVAQHSADLL GREKSDFLND VPEMKAHSEK VQSIPOIKKW IETRPASDW

**Spliced mRNA**

ATGGTTTCCT ACAAGCTTAC CTACTTCGAT GGACGCGGAG CCGGAGAGCT CTGCCGTCAA ATCTTTGCTG CCGCCGAGCA  
GAAATATGAA GATAACAGAC TTACCGATGA GGAGTGGGAG AAGTTCAAAG CGGCCGGAAA AACCCCATAAC AACCAAGCTTC  
CAATGCTCGA GGTAGATGGC AAACCACCTCG CTCAGTCCCA CGCGATGGCT CGTTATCTTG CTGGGGAAATT CGGGTTCAAC  
GGAAAGAGCA GATGGGAAGA AGCTCAAGTC AACTCCTTGG CCGACCAGTA CAAAGACTAT TACCGGGAGG CTCGTCCATA  
CCTCGCTGTG AAGCTTGGTT ACACAGAAGG AGACGCGGAG GCTCTTTACA CAAGCGTCTA TCTTCCAGTT TTCAAGAAAC  
ACTATGGATT CTTTGTCAAT GCTTTGAAGG CCAGCGGGTC AGGATTCTTG GTTGGAAATT CCTTGACTTT TATTGATTG  
CTTGTGCTC AGCATTCAAGC TGATTTGCTG GGACGTGAAA AGTCGGATCT TTTCAATGAT GTCCCAGAGA TGAAGGCACA  
TTCCGAAAAA GTTCAGTCAT TTCTCAGAT CAAGAAATGG ATTGAGACTC GTCCAGCGAG TGACTGGTAA

**FIG. 14**



The F11G11.2 gene is located on chromosome I. Regulatory sequences can be found e.g., in the region between 4 880 968 and 4 882 068. An exemplary sequence in or around this region is as follows:

AATTGAAATGAGTTGCAATTTGTATTATTTTAATTCAATTTCAAGAAGCAATTTTGCTAATTTGTTTAATGG  
 AAATCGATGTTCTAAAATATCTTGAATGAATTGTTCTTTAAAAATTATGGTAAAGTTTCAGCAGGATGTTCTAT  
 AGAAGCTTTGCATTGCAAGAGTGTGAAATATACAGGATATTACAAAAGCCTGGGAAGTAGGCATGCTTTAGGTAC  
 AAATCAGACCTACACCGCCTCCTTGTGGTTACCATCATAGCTAAAACCTTCCGAACATTCCCTGGTGAGACACAATG  
 TTCAAAGCACAAAACCAATCACGTATAATGTTAATTGACTTTATTGTCAAAAATTACAAAAGCGTCGTTCTGGAA  
 CATGAACATAATAAGAATTTCAAATT CGGTGGGACAATAAATATGTAATCTTTATTATTTGGAGGATAGTCTT  
 TTCAAAGGCAGGTGTATAACCCTCAAAAGAAAGCACGTTGTGTTCAAAGTGAGACTAAATTATTCAAAGACAAATT  
 CCATAGGAAATCATTGTCATCAGGCACCTCCAGAAATTAGGCTGTAGGCAGGCACGTAGGCTGCGTAAATGCCTAC  
 GCCTCTTTGCGCGAGATTATGAAATTGTGTTACTGTGCGAAAAATTTCAGAAACAAAAAAATATTTTGACT  
 TTTGTGTCAGTTAGTAGTTCTTATCATGGTATCTCAATAATAATGGCAAGCGTAAC

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AAGATGATTGATGCCATGGTTATATTGTGAGTAGTCACAAATTGTGACACAAACATTCCCTCGAAAGATCTGGAAAA  
 GTCACAAAACCTTGCATATATTTTCAACCAATATTATTTGACCTACTCTGTTCATCGTAACATTGCAACAAACAAAA  
 AACGATGACTACACTTATGATTCTAGTCAACAAACGTGCGCGCAATGTGTAGAGCAAATGATGACAAACTACAGAATAT  
 GGTGAGTGGAGAGACGACAGACATTGAGAAATGGGTATAAATA

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GAGACGGCCGGCATTCAACCTCTCATCGACCACTCGATTCTGCTTGGTTATTCACAAATG

FIG. 15

Exemplary F11G11.2 (gst-7) sequences:

**Amino Acid Sequence**

MVHYKVSYFP IRGAGEIARQ ILAYAGQDFE DNRIPKIEWP AVKPSTPEQG LPLLEVDGKV LAQSHAIARY LARQFGINGK CAWEEAQVNS VADQFKDYLN EVRPYFMVKM GFAEGDLDAL AKDVFPLPGFK KHYGFFANFL KSAGSGYLVG DSLTFVDLLV AQHTADLLAA NAALLDEFPO FKAHQEKVHS NANIKKWLET RPVTPF

**Spliced mRNA**

cgaccactcg atttcttgct tggttatttc aacaATGGTC CACTACAAGG TATCGTACTT CCCAATTCTGT GGAGCTGGAG AGATTGCTCG TCAGATCTTG GCCTACGCTG GACAAGACTT CGAGGACAAC AGAATCCAA AGGAGGAATG GCCAGCTGTC AAGCCAAGCA CTCCATTCTGG ACAGCTTCCA CTCCTTGAAG TTGACGGAAA GGTTCTTGCC CAATCTCATG CTATGCCCG TTACTTGGCT CGTCAGTTCG GAATCAATGG AAAGTGTGCA TGGGAGGAGG CTCAAGTCAA CTCGGTTGCT GATCAATTCA AGGATTACCT CAACGAAGTT CGTCCATACT TCATGGTGAA GATGGGATTT GCTGAAGGAG ATCTCGATGC TCTTGCCAAG GACGTCTTCC TTCCAGGATT CAAGAAGCAC TATGGATTCT TTGCTAACTT CCTCAAGTCG GCTGGATCG GATACTTGGT TGGAGACTCT TTGACCTTTG TCGACTTGCT CGTCGCTCAG CACACTGCTG ATCTTCTGGC TGCCAACGCA GCTCTTCTCG ATGAATTCCC ACAATTCAAG GCTCATCAGG AAAAGGTTCA CTCGAATGCC AACATCAAGA AGTGGTTGGA GACTCGTCCA GTTACTCCAT TCTAAatgat ttcca

**FIG. 16**

The K08F4.7 gene is located on chromosome IV. Regulatory sequences can be found e.g., in the region between about 10141800 and 10142217. An exemplary sequence of this region is as follows:

ATTATCAAAAAGATTAGAAGTTGGCAAACCTGGCAAGAATTCCAGAGATTGCACTAAAGTTGTAGCCAAGTTGAT  
CCAACCTTATCCAATCTTTACTAAAATTATCCTTAAGACTATTAAATTAGATAGAGAATTGGCGAGAGTTAGATCC  
CACTTGATATGACTTATAGTTAGCCTAACCTGAAGCTATTGCTTGCTGATCATTGGTTATCGCTTGCTACTTGG  
TAACCAGCTCCAATAGTTGTTATTTGCTTTGTCATCATT

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TCCACGATTTACACTCTCAAGTGAACCAACTGTTCTTGATGCCAGACGATGACATTACACTTGATAAGA

-83

AAATATATATAAACTGGAATTAAAAACAATTGATACATCGATTCAATTACTGAATTCTAATTATG

**FIG. 17**

### Exemplary K08F4.7 (gst-4) sequences:

## Amino Acid Sequence

MPNYKLLYFD ARALAEPIRI MFAMLNVPYE DYRVSVEEWS KLKPTTPFGQ LPILQVDGEQ FGQSMSITRY LARKFGLAK  
TAEEEAYADS IVDQYRDFIF FFRQFTSSVF YGSDADHINK VRFEVVEPAR DDFLAIINKF LAKSKSGFLV GDSLTwADIV  
IADNLTSLK NGFLDFNKEK KLEEFYNKIH SIPEIKNYVA TRKDSIV

## Spliced mRNA

ATGCCAAACT ATAAGCTATT GTATTTGAT GCTCGTGCTC TTGCTGAGCC AATCCGTATC ATGTTTGCAA TGCTCAATGT  
GCCTTACGAG GATTATAGAG TTTCAGTGGAA AGAATGGTCA AAGCTGAAGC CAACGACTCC ATTTGGCCAG CTTCCCATT  
TACAAGTCGA TGGAGAACAA TTCGGTCAGT CAATGTCTAT CACAAGATAC TTGGCAAGAA AATTGGACT CGCTGGAAAA  
ACTGCAGAGG AAGAAGCTTA CGCTGATTCA ATTGTAGATC AATACAGAGA TTTCATATTTC TTTTCCGTC AATTCACTTC  
TTCCGTTTTC TATGGAAGTG ACGCTGATCA TATTAACAAA GTACGTTTG AAGTTGTTGA ACCAGCCCGT GATGATTCT  
TGGCAATAAT CAATAAGTTC CTGGCCAAGA GTAAATCAGG ATTCCCTCGTT GGAGACTCAT TGACTTGGGC TGATATTGTG  
ATTGCTGACA ATTGACAAG TCTCCTGAAG AATGGATTCT TAGATTCAA CAAAGAAAAG AAGTTGGAAG AGTTCTATAA  
CAAGATTCAT TCAATTCCAG AAATTAAGAA TTACGTGGCA ACAAGAAAGG ATAGTATTGT TTAAAatcga attattttaag  
tctgaattat gtatgttagta aaataatatc gttcctatca cgtctcccg agagcgtaat aaatttattat tatgtg

**FIG. 18**

The *sod-1* gene is located on chromosome II. Regulatory sequences can be found e.g., in the region between about 6 973 806 and about 6 974 406. An exemplary sequence of this region is as follows:

```
ATTCCGCAACCCCGTCAAATTAAAGAAGAGAAAGAAAAAAACACAACGTGTTGCACCTGTAAGGTAGT
TTTTTTTGTGCCTCGGCCTTGATTCACATGAAAGTTCTACGGAAAAACTTCATTGCATAACGA
TCTTCATATCTGTTCTGGAAACGAAAATTCCAACATGAAAGAAACCCGACGCTATTATTCTCGCAA
CACAAAAATTTCACATTAAACCGCGGTTTCTCGAACAGCATATTGACGCCATTGCTCGTCAA
GTTTGATGCGTGCACACTATTGCTGTTTTCTCTAAATTCTTACGCTTCGTA
GTTTCTATAGAAACGATTCTCACTCCCGGTTTCTCCGATTCTCAAAATTAAATTAAAATTAGTTATT
AAAAATCCTTTCTTGAAATAATCGTTCAATTGAGTTCAAGAGTGGAGACGTTGAATTGTGAGC
CGCTTATTTCTGTGTTGTTAATCAGTGTCATAATCATAACTTCCATTGTTCT
```

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TTATTATTCAAAGTTGTAGATTCAAGTATTAGATCGGTGATG

**FIG. 19**

Exemplary sod-1 sequences:

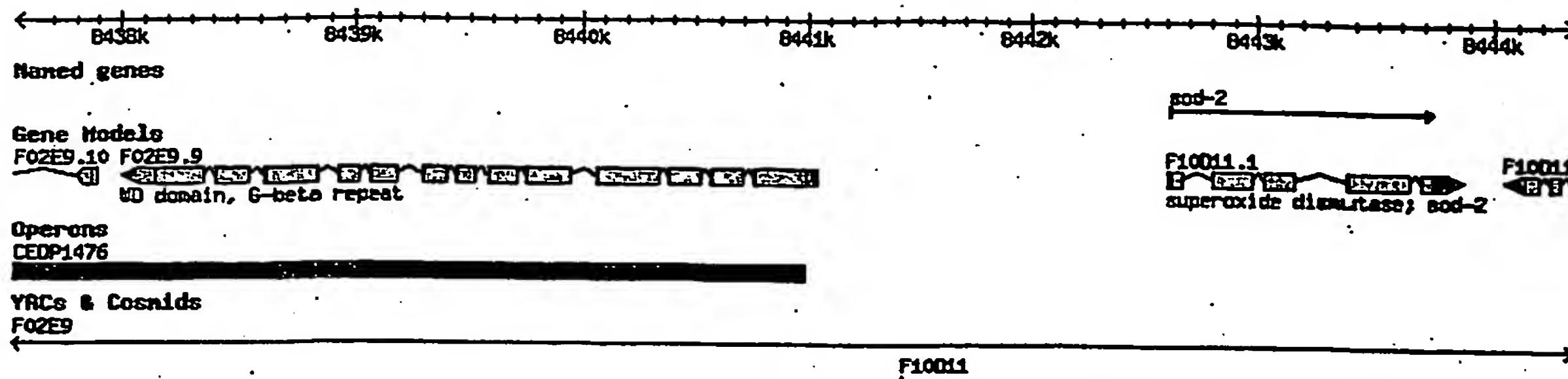
**Amino Acid Sequence**

MFMNLLTQVS NAIFPQVEAA QKMSNRAAVV LRGETVTGTI WITQKSENDQ AVIEGEIKGL TPGLHGFHVH QYGDSTNGCI  
SAGPHFNPFG KTHGGPKSEI RHVGDLGNVE AGADGVAKIK LTDTLVTLYG PNTVVGRSMV VHAGQDDLGE GVGDKAEESK  
KTGNAGARAA CGVIALAAPQ

**Spliced mRNA**

tttagatcg tgATGTTAT GAATCTTCTC ACTCAGGTCT CCAACGCGAT TTTCCGCAG GTCGAAGCCG CTAAAAAAAT  
GTCGAACCGT GCTGTCGCTG TTCTTCGTGG AGAAAATGTT ACCGGTACTA TCTGGATCAC ACAGAAGTCC GAAAATGACC  
AGGCAGTTAT TGAAGGAGAA ATCAAGGGAC TTACTCCCGG TCTTCATGGA TTCCACGTTT ACCAATATGG TGATTCCACC  
AACGGATGCA TTTCTGCCGG TCCACACTTC AATCCATTG GAAAGACTCA TGGTGGACCA AAATCCGAGA TCCGTCACGT  
AGGCGATCTA GGAAATGTGG AAGCTGGAGC CGATGGAGTG GCAAAAATCA AGCTCACCGA CACGCTCGTC ACGCTTTACG  
GTCCAAACAC TGTGTTGGC CGATCTATGG TTGTTCATGC CGGACAAAGAC GACCTCGGCG AGGGAGTCGG AGACAAAGGCA  
GAAGAGTCCA AGAAGACTGG AAACGCCGGA GCTCGTGCTG CCTGCGGTGT CATTGCTCTC GCTGCTCCCC AGTGActacc  
tgaatcgctt ctctgaatct ccacacaaatt cctactaaag acaattttc atttcttgct ttgtcgttat attcttaaga  
atcccgttgc tcctactcct actactgtat atttcacat aaaatttctt caaaatttca aataaagggtt gtatgttc

**FIG. 20**



The *sod-2* gene is located on chromosome I. Regulatory sequences can be found e.g., in the region between about 8 441 038 and 8 442 612. An exemplary sequence of this region is as follows:

TGAATAAAAACGTTAACCCAACGGACATCAAAGTATCAAAGTAAGTAAGTAACCTGAATAAAAACGTTGCA  
 TATAAAAAATCTACTCGAAAATTAAAGTGAGATTGAAGGATTGCTTCCGAAGAGAAAATGACAATTATAGGGTATACTA  
 AAACATCAAAATGTATATTAGACTACCATAAAATATAAAACATCAGTGCTGCTCTCCAAGCTATTCTGACGGATTGCGAC  
 AACGAGCTCGCTGGAGTTGGCATCAGTGTGGAAGGCAGACACATAAGAAGACTCGAATTTCGCGGATGACGTAGTCCTGAC  
 ATGTTCCACACCGGGAGAAGTTCAAGAACGACTGGAAATTGGACCGAATAAGTTCTAATTACGGACTCAAGATCAATC  
 AGTCAAAGACTGTTCTCTGAAGAACAAAGTTGCCGGAGCCAAGACGTCCCTTTCAACGGATCCCCATCATTCCGTG  
 CCTGGTTGCCGCTATCTGGGTCGCTGGATCGACATTCTGGCTCAATTGACGAAGAGATCTCGAGGAGAATAAGAGCAGG  
 TTGGGGTGTCTGGTTGGAATCAAAGAAGTCTTGAGAATCATGCCAACAGGAAAGAATCATCCTCTCAAGCAAAAT

-980

-959

GTGCTACCAAGCTCTCTGTATGCTAGTGAAACTTGGACTTGTAAATGCTGGATCCACGTTGAGACTCAAAAGAACTGTCAC  
 CGGTCTCATCGACGCTGCAGAAATTGAGGCTGGAACCTCAACTTGGAACGTACCTCCTGCAAAACAATCAAGATTG  
 CAGGACACATTCTACGGAGAGATCCAAACCGATGGACAAAAATCTGCAACGGAATGGGACCGGAGCCACAACAAAAATTGG  
 AAACGTGCCGTTGGAGGACAGAAGAGATGGGCTAAGGACATCGACGAAGAACGCAAAATTCCACCACAATTCCGC  
 CATGTCGGGACAAGTCGTTGGAGAAGAACGACTAGGAATGCTCACTCCGAAGGCTCCATGGCTGTCCATCGCACGAA  
 CCGACCGTAAAAATGGAAAGAGTTGTCGCAAGTGGCTCGCAACTTGAACCCAACGGACATCAAAGTATCAAAGTAAG  
 TAAGTAAGTAAGTAACCTGAATAAAACGTTGCAATTAAAGTACTCGAAAATTAAAGTGAGAATTGAAGGATTGCTT  
 TCCGAAGAGAAAATGACAATTATAGGGTATACTAAAACATCAAATGTATATTAGACTACCATAAAATTACGATAAT

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TTAAAAAATTACTAGAAACACGCAATTGGCTCAAAAGCAACAATTAGACTGAAAACGAGCTAAAGAATATTATTC  
 AAACCACTTGCTCGTAAATCTGGTGTATCATGTTCCGCAACACTGTCTTTGTTGCG

-191

TACTTGTGTTACGCGATTGAAATTCACTGTTGCTTTGTTACTTTTATTTCATCCAAAATCGTATTT  
 CAGCTTGATATGTTCTGCGAATTGAAATTATTTGACTATTGAATATTAAATTGAGCCGAAAATG

Exemplary sod-2 sequences:

**Amino Acid Sequence**

MLQNTVRCVS KLVQPITGVA AVRSKHSLPD LPYDYADLEP VISHEIMQLH HQKHHATYVN NLNQIEEKLH EAVSKGNVKE  
AIALQPALKF NGGGHINHSI FWTNLAKDGG EPSAELLTAI KSDFGSLDNL QKQLSASTVA VQGSGWGWLW YCPKGKILKV  
ATCANQDPLE ATTGLVPLFG IDVWEHAYYL QYKNVRPDYV NAIWKIANWK NVSERFAKAQ Q

**Spliced mRNA**

tttgcagccg aaaATGCTTC AAAACACCGT TCGCTGTGTC TCAAAGCTTG TTCAACCGAT CACAGGAGTC GCTGCTGTTC  
GCTCGAAGCA CTCGCTGCCA GATTTACCAT ACGACTATGC TGATTTGGAG CCTGTAATCA GTCACGAGAT TATGCAACTT  
CATCATCAAA AGCATCATGC CACTTATGTG AACAAATCTCA ACCAAATTGA GAAAAGCTT CACGAGGCGG TCTCCAAAGG  
AAACGTCAAA GAAGCTATCG CTCTTCAGCC AGCTCTCAAG TTCAATGGAG GAGGACATAT CAACCACTCC ATCTTCTGGA  
CTAATTTGGC AAAGGACGGA GGAGAACCAT CGGCAGGAGTT GTCACCCGCA ATTAAGAGCG ACTTCGGATC TCTGGATAAT  
CTTCAAAAAC AGCTTCGGC ATCAAATGTC GCTGTTCAAG GATCAGGATG GGGATGGTTG GGATACTGTC CAAAGGGAAA  
GATCTTGAAG GTTGCACAT GTGCCAATCA GGATCCACTT GAGGCAACAA CTGGACTTGT TCCACTGTC GGAATTGACG  
TCTGGGAGCA CGCTTACTAC TTGCAGTACA AGAATGTTCG ACCAGATTAT GTCAATGCTA TTTGGAAGAT CGCCAACCTGG  
AAGAACGTCA GCGAGCGTT TGCAAAGGCA CAGCAATAAa tgagctgaat cacaagaatt aatcgtaaaa tgttagcaga  
gaagttgact cccatttttt tgtaactatt tttgtttctt aattatttcg aaatgtaaat tttcaaacct tttcaaatga  
aaagtttca ccg

**FIG. 22**

The *ctl-1* gene is located on chromosome II. Regulatory sequences can be found e.g., in the region near 14 306 135. An exemplary sequence of this region is as follows:

AAAAAAAATCGATAAAAATCCCGTCAACGAAAGTTAAAGTTACAGTATTGTCGTTCGAGACCGG  
GTACCGTAGTTTGGTAAAACATTGCAAAATTGGTCAACAATTTCATCGCTGCGAGACCGACACAAC  
ACTTTATTTATTTGGTTCCCTATCGCTTATCATAAACATGTGACGTCATCTCTTGTACAGA  
-997 -978

GCACCGCGACTGGGAGTATAAGAATGCCGGAAAACATCAATAATCAGTTGGTAGAAGTAAAATTGAG  
CGTAAAATATGATCATTTCGATGCACCATATTGACGCGAATACTCTACAAGCCGCTGTACTGC  
-880

TCGTGGACAACTTGGATTATTTTTGTTTAAAATTCAAAATAGTCAATATATTGCTTATTATAGCG  
CGCCTTTTGACAGTAAGTTGTCAAATTGCGCGTAAGTTATGGTGTGCACATATGCACCATACAGC  
AACACCCCGCGGCCGGCTAGGGTACATCCATGCAAATGCCTCTACTGATAATTGAGTTAACCAAGG  
TTTAGGGCAAGATAAGAAAAAGCTTGGACCAAAAAATTAGAGTTATTTTCGGACATTTTA  
TATACATCACAAAATATTGGGCCACTCGTTTGATAAAAACGACAAGCCAAAAGTTCAAGGTATACGG  
TAGACAAATTGCGTACAGGTACCACTTTCCACGTAGTGCCAGGTTGCCATTACGCTTGATCTATGA  
AAAATGCGGAATTTCGTCCAGAAAAATGTGACGTCAAGCACGTTCTCAACCATTGCGAAATCAGTTGAA  
AACTCTGCGTCTATTCTCCGCATTTTGATCTGTAGATTGTAGATCAATCCATTCCCCGTATAC  
CCTGACCCATAATCAATACCTACCTAATTTGTCTTCCCTACTTTTGCGCTGTCCAAAATAAGCG  
AGACTATGCCGTAGTCTGGTGTCCAACAACATGTTCTTACGTGATAACGCTACAATCTCTTCTT  
TTTCTCTGTTCTCTGTCTCCAAACCATATTCCGTATTACACCTCGTGGTCATTTTTGTTC  
AGAGTTTATTAAATTCTAACTAAAATTCTAACTAAAATTCTAGA

FIG. 23

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Exemplary ctl-1 sequences:

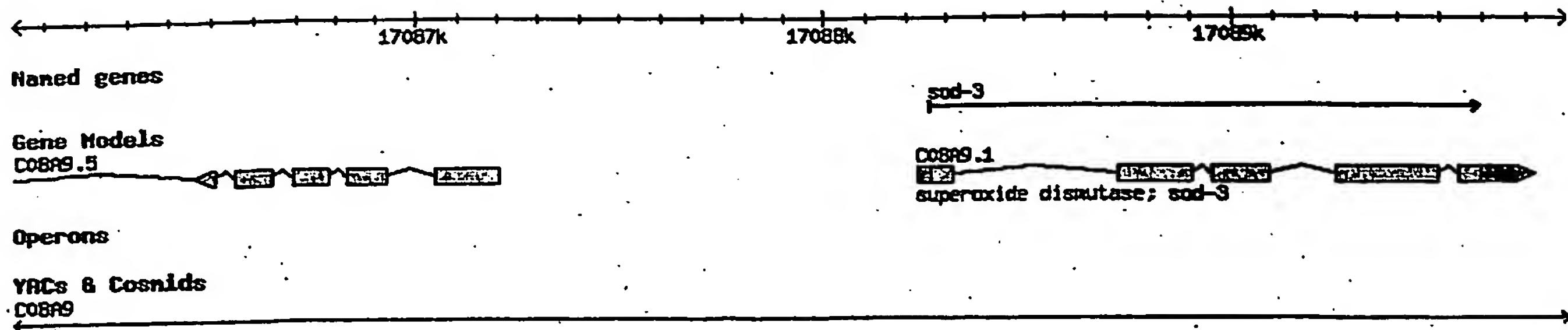
## Amino Acid Sequence

MPNDPSDNQL KTYKETYPKP QVITTSNGAP IYSKTAVLTA GRRGPMLMQD VVYMDEMAHF DRERIPERVV HAKGAGAHGY  
FEVTHDITKY CKADMFNKVG KQTPLLVRFS TVAGESGSAD TVRDPRGFSL KFYTEEGNWD LVGNNNTPIFF IRDAIHFPNF  
IHALKRNPQT. HMRDPNALFD FWMNRPESIH QVMFLYSDRG IPDGFRFMNG YGAHTFKMVN KEGNPIYCKF HFKPAQGSKN  
LDPTDAGKLA SSDPDYAIRD. LFNAIESRNF PEWKMFQVM TFEQAEKWEF NPFDVTKVWP HGDYPLIEVG KMVLNRNVKN  
YFAEVEQAAF CPAHIVPGIE FSPDKMLQGR IFSYTDTHYH RLGPNYIQLP VNCPYRSRAH TTQRDGAMAY ESQGDAPNYF  
PNSFRGYRTR DDVKESTFQT TGVDVDRYETG DDHNYEQPRQ FWEKVLKEEE RDRLVGNLAS DLGGCLEEIQ NGMVKEFTKV  
HPDFGNALRH QLCQKKH

## Coding

CTGAAAACCT ACAAGGAGAC GTATCCAAAA CCCCAAGTGA TCACAACCTC AAAATGGAGCT CCGATCTACT CGAAGACCGC  
CGTGCTCACC GCCGGGCGGC GTGGCCCAAT GCTCATGCAA GATGTAGTTT ATATGGATGA GATGGCTCAT TTCGATCGTG  
AACGTATCCC CGAGCGTGTGTC GTTCATGCCA AGGGAGCCGG AGCCCATGGA TACTTCGAGG TCACCCATGA CATCACCAAG  
TACTGTAAGG CCGATATGTT CAACAAGGTC GGAAAACAGA CACCACTTCT CGTTCGTTT TCAACGGTCG CTGGAGAAC  
GGGATCCGCT GATACTGTCC GCGATCCACG TGGAATTCTCT CTCAAATTCT ATACCGAGGA GGGTAACTGG GATCTGGTTG  
GAAATAACAC TCCGATCTTC TTCAATTGTG ACGCAATCCA CTTTCCGAAT TTCAATTCTG CCCTGAAGCG CAATCCACAG  
ACTCACATGA GGGATCCGAA TGGCCTCTTC GATTCTGGA TGAATGCCCT TGAATCCATT CATCAGGTGA TGTTCCCTCTA  
CTCGGATCGT GGAATTCCCTG ATGGATTCCG TTTTATGAAT GGATACGGAG CGCATACTTT CAAGATGGTC AACAAAGGAGG  
GAAATCCGAT TTATTGTAAA TTCCATTTCAG AGCCTGCTCA AGGTTCCAAG AATCTCGATC CAACTGACGC TGGAAGCTC  
GCCTCTTCGG ATCCAGACTA TGGCATTCCGC GACCTGTTCA ATGCCATTGA GTCAAGAAAT TTCCCGGAAT GGAAGATGTT  
CATTCAAGTG ATGACATTCTG AACAAAGCTGA GAAATGGGAG TTCAATCCAT TTGATGTCAC TAAAGTTGG CCACACGGT  
ATTACCCACT GATCGAGGTC GGCAGAGATGG TGCTGAACAG GAATGTGAAG AATTATTTCG CTGAGGTGCA ACAAGCCGCC  
TTCTGCCCGG CCCACATCGT CCCAGGAATC GAGTTCTCGC CAGACAAAGAT GCTCCAAGGG CGTATCTTCT CCTACACGGA  
CACGCATTAC CATCGCCTTG GACCAAACTA CATTCAAGCTT CCAGTCAACT GCCCGTACCG CTCCCGTGT CATAACACTC  
AACGCGATGG TGCAATGGCT TATGAAAGCC AGGGAGATGC GCCGAATTAC TTCCCGAACA GTTCCCGGG ATACCGTACT  
CGTGATGATG TGAAGGAGTC GACATTTCAAG ACCACTGGAG ATGTTGATCG TTATGAGACT GGAGACGATC ACAACTACGA  
GCAGCCACGT CAGTTCTGGG AGAAAGTGCT CAAGGAGGAG GAGAGAGATC GGCTCGTTGG GAATTGGCT AGTGATTTGG  
GTGGCTGTTT GGAGGAAATT CAAAATGGAA TGGTCAAAGA GTTCACGAAA GTTCATCCGG ATTCGGAAA TGCTCTTCGC  
CATCAGCTCT GCCAGAAGAA GCATTAAatt

FIG. 24



The *sod-3* gene is located on chromosome X. Exemplary regulatory sequences include:

TATTCGCAGAAAAAGTCGGCAACATTGTTTATATGTTTCTTGAGAAAGCGTGGTCATT  
 TTGAAAGTAAAAATATTGCTTAAACTTCAAATTAAATCTGCAGTGATTAGAGAGGTTGAGAATT  
 ATTTCAAAACATTCAATGTTCCCTGGAGTGACTATGCAAATATGAAAATGTTCCAAAAATATT  
 TGGATGCCCTGATAAAAGTAGGTGAAATTTCGAGGGAACATCATATTAAAATGTTGAATTAGAA  
 GAAATGAAATGTTGCGGTGGTATGCTGAATATTGAGATATTATATTTACTGTTAAATCCGAAA  
 TTTTGACAAACGGAAAAATTGTCGAAATACTACATTTCGATAACACAAAGGTACTCCATAACA  
 CTTATAAAACTGTTGACTATCTTATTCAAGGAAAAAAATCCAAGAATAAACATTTCAGAATTG  
 AACATTCTAATGGCTGATTAATAAAACAAAGTTATACAACATTCAAAGCAGTTGCTCAATCTGGCATT  
 TCTTGTTTTGAATATTCACTCAGCAAGATGTTGATAATTGTTAATTCTAATTGTTCT  
 ACAATTTCAAACCGAAAATTGACCTTGACTTTGTTACTTTGTTCTCGTGGGTTAACTGTTCACTGA  
 TTTCTATTGCTGTTGATGAGGTCTTGATCAAATTGTTACTGCATATTGCTCAATTCT  
AAATCATCTAATATATTGTCAAACAACTTCTGTTTTTCAATTCAAACCTCTGCAAAACGTTCT  
 -287

CTTAACAAAGGTTCACACAACACTCTCCTCTCCATCTCTCAACAAACAATGTGCTGGCCTTGCA  
 TGTTGCCAGTGCAGGGTTGTTACCGCTTCAAGATTTGGTCTCCTATCTAACGTCCCAGGAAATGCAT  
 TTTTCCTTCATTGGTTTTCTGTTGAGAAAAGTGACCGTTGTCAAATCTCTAATTTCAGTG  
 AATAAAATGCTG

FIG. 25

Exemplary sod-3 sequences:

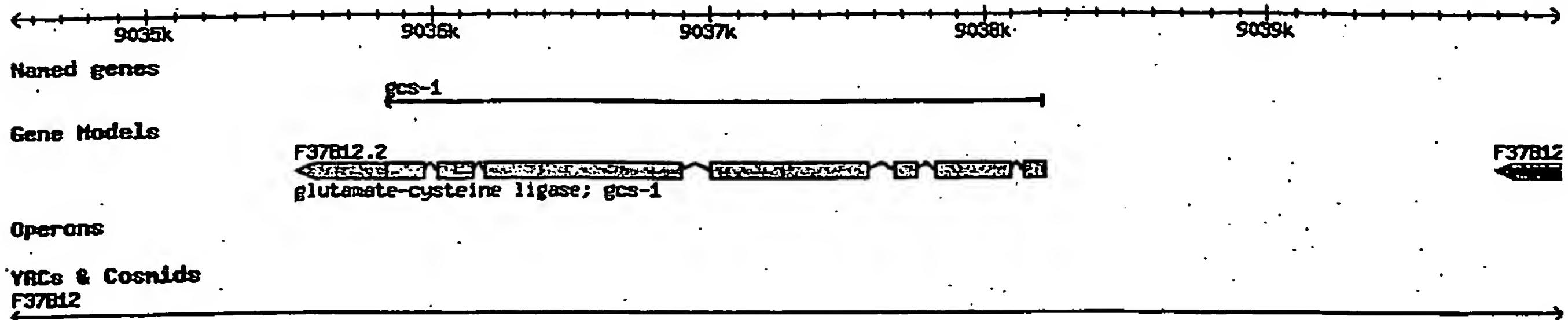
**Amino Acid Sequence**

MLQSTARTAS KLVQPVAGVL AVRSKHTLPD LPFDYADLEP VISHEIMQLH HQKHHATYVN NLNQIEEKLH EAVSKGNLKE  
AIALQPALKF NGGGHINHSI FWTNLAKDGG EPSKELMDTI KRDFGSLDNL QKRLSDITIA VQGSGWGWILG YCKKDKILKI  
ATCANQDPLE GMVPLFGIDV WEHAYYLQYK NVRPDYVHAI WKIANWKNIS ERFANARQ

**Spliced mRNA**

cgtttgtcaa atcttctaat tttcagtcaa taaaATGCTG CAATCTACTG CTCGCACTGC TTCAAAGCTT GTTCAACCGG  
TTGCGGGAGT TCTCGCCGTC CGCTCCAAGC ACACTCTCCC AGATCTCCC TTCGACTATG CAGATTGGA ACCTGTAATC  
AGCCATGAAA TCATGCAGCT TCATCATCAA AAGCATCATG CCACCTACGT GAACAATCTC AATCAGATCG AGGAGAAA  
TCACGGGGCT GTTTCGAAAG GGAATCTAAA AGAAGCAATT GCTCTCCAAC CAGCGCTGAA ATTCAATGGT GGTGGACACA  
TCAATCATTC TATCTTCTGG ACCAACTTGG CTAAGGATGG TGGAGAACCT TCAAAGGAGC TGATGGACAC TATTAAGCGC  
GACTTCGGTT CCCTGGATAA CTTGCAAAAA CGTCTTCTG ACATCACTAT TGCGGTTCAA GGCTCTGGCT GGGGATGGTT  
GGGATATTGC AAGAAAGACA AAATCTGAA GATGCCACC TGTGCAAACC AGGATCCTT GGAAGGAATG GTCCCACTT  
TTGGAATTGA CGTTTGGGAG CACGCCTACT ACTTGCAGTA CAAAAATGTC CGCCCGACT ATGTCCATGC TATTTGGAAG  
ATTGCCAACT GGAAGAATAT CAGCGAGAGA TTTGCCAATG CTCGACAATA Aaagcaggaa atattgaaat tttcggttt  
acgaaaatat tgaagataat tcagatgtag tttaaaacgc tgagaatttg tattttgtat attgtttaaa taaaagaacg  
cacagtttt tctta

**FIG. 26**



The *gcs-1* gene is located on chromosome II. An exemplary regulatory sequence is:

TTATCAACCACTAGGTTCCGTCTTAATCGTCCAAATATTGATCCGCTCGCTCGTGTCTCAACTCTTTATTTGCTGT  
 GTTTTCTGTTCTATAGTTCTCCATTTCCATCTCCTCTCGCTTGTGAATGGACTTATTTGATAAGTTCATTTA  
 ATTTTCTAACAACTCATCACTAGCTCATGATGACAATTGCAAAGAAATTCGTCATATAGAGGGGAAAAATGCTGACAA  
 -607

ATATTGAAAAGCCTTCAGGAGAGATGTAGAGACGTAGGAGTAGAGACAGAACATAAAATTGAGAAGCTTGTAGGGAGAAT  
 AGACATAGAGTTACCATGGGAAAACGCTCGCATTTCATTTCCATTAAACGAGATTCTAGATCACAAACATTTGTGATCCGT  
 TGTGCGAAAATCAAGCTTTATCAAACTTTATCGTCTGTTCATTCTTCTGACAATCTTATTATCTTATTAAACTTG  
 ACTAATTGTATTGAAAGTATTTTAGATGCGAACGAAGTCCATTTCATGACTTAACATCTTAACGTTAGTGAA  
 -316

ATTTTGAAATTCCAATTAGGACTACGGTAGGAGTTCTGTAGTTGATTCTGAACACTGTTGTAAACCTTCTGAACG  
 GATTTAATATTCTAAAATTGCAAATCTGAGTCCTATTAAAGATGTTCATCCGTAAAACCAACAAACAAA  
 ATATCACTTATCATGAGATTAAATGTTCTTTGATTCTGAATTGTTGTACTTCCTTCAAACGACTTATTGA  
 -121

ACTGATGTAACCTTCCTTCTAATGTTATCATTGTATTTTGCAAGAATG

FIG. 27

Exemplary gcs-1 sequences:

**Amino Acid Sequence**

MGLLTGSPL TWAETVPRID YIKKHGIAQF INLYHRLKSR HGDQLKGDE IEYTIVKFDD ANKKVRVSCK AEELLNKLQA  
 EEQVNAMLGT ANRFLWRPEF GSYMIEGTPG MPYGGGLIACF NIVEANMKLR RQVVKLLKK DETCLSISFP SLGVPGFTFP  
 EVAADRKNDD AANSVFWPEQ AVFLGHPRFK NLTKNIKGRG GSKVAINVPI FKDTNTPSPF VEDLSALGGP DDTDRDAKPDH  
 IYMDHMGFGM GCCCLQVTFO AVNVDEARWL YDQLTPITPI LLALSAATPI FRGKLSNVDS RWDIISASVD DRTPEERGILE  
 PLKNSKWVID KSRYDSTDY IYPCSVGYND IPIQYDETIY KQLIDGNIDE PLAKHIAHMF IRDPHQVFRE RIEQDDEKSS  
 EHFETIQSSN WMNMRFKPPP PDAPEIGWRV EFRPTEVQLT DFENAAYCCF VVLTRMMIS FRLTYLMPIS MVTEMNKRAQ  
 QKDAVLNQKF LFRKGLAEC SAPENLKGSE KCGPPSQDIE EMSIDEIING KKNGFPGLIS LIRQFLDSAD VDVDTRCTIS  
 QYLNFISKRA TGEINTLAHW TRGFVQSHPA YKHDSDVNDN IVYDLLKKMD AISNGEDHCE KLLGCYRSKT DHAISAAVRK  
 AEEHMIVSSQ KRAH

**Spliced mRNA**

tttgcagaAT GGGCTTTG ACGAAAGGTA GTCCGTTGAC GTGGGCAGAA ACCGTACCGC ACATTGATTA TATCAAGAAG  
 CACGGAATTG CTCATTCTAC CAATCTCTAC CATCGTCTGA AATCAAGACA CGGAGATCAA TTGAAATGGG GAGATGAGAT  
 TGAATACACT ATTGTAAAAT TTGATGACGC AAACAAGAAA GTTCGCGTGT CGTGCAAAGC TGAAGAGCTT CTTAATAAGT  
 TACAAGCCGA AGAGCAGGTG AATGCGATGC TTGGAACTGC CAATCGATTC CTTTGGAGAC CAGAATTCCGG ATCCTACATG  
 ATCGAGGGAA CCCCCGGAAT GCCTTACCGA GGTCTCATCG CTTGCTTCAA CATTGTCGAG GCAAACATGA AATTGCGCAG  
 ACAGGTCGTC AAAAAGTTAT TAAAGAAGGA TGAAACATGT CTATCGATAT CGTCTCCATC TCTTGGAGTA CCTGGATTCA  
 CATTCCCGGA AGTAGCAGCT GATAGAAAGA ATGATGATGC AGCTAATAGC GTTTCTGGC CAGAACAAAGC TGTATTCTG  
 GGCCATCCAC GTTTCAAGAA TCTTACAAA AATATTAAAG GTCGCAGAGG AAGTAAAGTA GCTATCAACG TCCCGATATT  
 CAAGGATACG AACACCCCCA GTCCATTCTG TGAAGATTAA TCTGCACTG GAGGTCTG TGATACTCGT GATGCGAAC  
 CTGATCACAT TTATATGGAT CATATGGAT TCGGAATGGG GTGCTGTTGT CTTCAGTC CTTTCCAGGC TGTGAACGTC  
 GATGAAGCCA GATGGTTGTA CGATCAGCTG ACACCGATTA CACCGATTCT ACTGGCCTC TCTGCCGCC CACCAATCTT  
 CCGTGGAAAA TTATCCAATG TCGATTCTAG ATGGGATATC ATTAGTGCAA GTGTCGACGA TCGTACACCG GAGGAAAGAG  
 GATTGGAACC TCTCAAGAAT TCGAAATGGG TTATTGATAA GAGTCGCTAC GACTCCACGG ACTGTTACAT TTATCCATGT  
 TCTGTTGGCT ACAATGATAT TCCTCTTCAA TACGACGAAA CCATATATAA ACAACTAATT GATGGAAATA TTGATGAGCC  
 ACTGGCAAA CATATTGCGC ATATGTTCAT TCGTGATCCA CATCAAGTT TCCGTGAGCG TATCGAACAG GACGATGAGA  
 AAAGCAGTGA ACACCTTGAA ACAATTCAAT CATCGAATTG GATGAACATG CGATTCAAGC CACCACCAAGC AGATGCTCCA  
 GAAATCGGAT GGAGAGTCGA ATTCCGGCCA ACTGAAGTTC AACTGACCGA CTTTGAAAAT GCAGCATACT GTGCTTCGT  
 TGTATTGCTC ACCAGAATGA TGATCTCCTT CAGGCTGACA TATTGATGC CAATTTCAAT GGTTACTGAA AATATGAAGC  
 GTGCTCAGCA AAAAGATGCA GTTCTCAATC AGAAATTCT GTTCAGAAA GGATTGGCTG AGTGCACATC TGCTCCCGAA  
 AATTTGAAAG GATCGGAGAA ATGTGGACCA CCTAGTCAAG ATATTGAAGA AATGTCGATT GATGAGATTA TCAATGGAAA  
 GAAAAATGGA TTCCCAGGTC TCATTTCACT TATTGCCAA TTTCTAGATT CTGCTGATGT TGATGTGGAT ACTCGGTGTA  
 CGATTTCCTCA ATATTGAAAC TTTATTCGA AACGAGCAAC TGGAGAGATT AATACTTTGG CTCACTGGAC ACGTGGATTG  
 GTACAATCTC ATCCTGCATA CAAACATGAC AGTGATGTAA ATGATAATAT AGTTTACGAT CTTTGAAAAG AGATGGATGC  
 CATCTCAAAC GGAGAAGATC ACTGTGAGAA GCTGCTCGGA TGCTACCGCT CTAAAACCGA TCATGCCATT TCTGCTGCTG  
 TTGCAAAGC TGAAGAGCAC ATGATCGTGT CCAGCCAAA ACGTGCACAT TAGgcataa ttgattgatt atgtgatttt  
 aatttattta tggtctatac gtcgtttc ccattccttc taggccttcc atgattcaca attttcgat gccatatacaa  
 tttagttggc catctacatt aaattactga tatgttgatg ctatTTCTA gtaagcagat gtcagtgtt agtaattcaa  
 aaatttaaac tctgaatttc taaatgcttg tttttgagt agtaggaatc agtacgaatg gtacattaaat ctgaaaataa  
 tttcatattt atgtacaatg ctcccctgaa tccatcatat aattattatc cgtgtt

T19E7.2c (spliced)

### T19E7.2c (conceptual translation)

MYTDSNNRNF DEVNHQHQQE QDFNGQSKYD YPQFNRPMGL RWRDDQRMME YFMSNGPVET VPVMPILTEH  
PPASPFGRGD STERPTTSSR YEYSSPSLED IDLIDVLWRS DIAGEKGTRQ VAPADQYECD LQTLTEKSTV  
APLTAEEENAR YEDLSKGFYD GFFESFNNQ YQQKHQQQQR EQIKPTLEH PTQKAELEDD LFDEDLAQLF  
EDVSREEGQL NQLFDNKQQH PVINNVSLSE GIVYNQANLT EMQEMRDSCN QVSISTIPTT STAQPETLFN  
VTDSQTVEQW LPTEVVVPNDV FPTSNYAYIG MQNDSLQAVV SNGQIDYDHS YQSTGQTPLS PLIIGSSGRQ  
QQTQTSPGSV TVTATATQSL FDPYHSQRHS FSDCTTDSSS TCSRLLSSESP RYTSESSSTGT HESEFYGKLA  
PSSGSRYQRS SSPRSSQSSI KIARVVPLAS GQRKRGGRQSK DEQLASDNEL PVSAFQISEM SLSELQQVLK  
NESLSEYQRQ LIRKIRRRGK NKVAARTCRQ RRTDRHDKMS HYI\*

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T19E7.2b (spliced)

### T19E7.2b (conceptual translation)

MSLPSDFASS LLASSTTNT TNTAPAAVNS FDEQEEESKK ILNMYLQMFN QQQVDQHGHH HQHPYAYSGV  
SSTFDRVFPY SNYAYIGMQN DSLQAVVNSNG QIDYDHSYQS TGQTPLSPLI IGSSGRQQQT QTSPGSVTVT  
ATATQSLFDP YHSQRHSFSD CTTDSSSTCS RLSSESPRYT SESSTGTHES RFYGKLAPSS GSRYQRSSSP  
RSSQSSIKIA RVVPLASGQR KRGRQSKDEQ LASDNELPVS AFQISEMSLS ELQQVLKNES LSEYQRQLIR  
KIRRRGKNKV AARTCRQRRT DRHDKMSHYI \*

T19E7.2a (spliced)

### T19E7.2a (conceptual translation)

MGSSRRQRS	TSATRRDDKR	RRRQCFSSVA	DDEEETTSIY	GVSSIFIWIL	ATSSLILVIS	SPSSNTSIQS
SSYDRITTKH	LLDNISPTFK	MYTDSNNRNF	DEVNHQHQQE	QDFNGQSKYD	YPQFNRPML	RWRDDQRMME
YFMSNGPVET	VPVMPILTEH	PPASPFGRGP	STERPTTSSR	YEYSSPSLED	IDLIDVLWRS	DIAGEKGTRQ
VAPADQYECD	LQTLTEKSTV	APLTAEEENAR	YEDLSKGFY	GFFESFNNNQ	YQQKHQQQQR	EQIKPTLEH
PTQKAELEDD	LFDEDLAQLF	EDVSREEGQL	NQLFDNKQQH	PVINNVSLSE	GIVYNQANLT	EMQEMRDSCN
QVSISTIPTT	STAQPETLFN	VTDSQTVEQW	LPTEVVVPNDV	FPTSNYAYIG	MQNDSLQAVV	SNGQIDYDHS
YQSTGQTPLS	PLIIGSSGRQ	QQTQTSPGSV	TVTATATQSL	FDPYHSQRHS	FSDCTTDSSS	TCSRLSSESP
RYTSESSSTGT	HESRFYGYKLA	PSSGSRYQRS	SSPRSSQSSI	KIARVVPLAS	GQRKRGGRQSK	DEQLASDNEL
PVSAFQISEM	SLSELQQVLK	NESLSEYQRQ	LIRKIRRRGK	NKVAARTCRQ	RRTDRHDKMS	HYI*

## Human Glycogen synthase kinase-3 beta (GSK-3 beta).

1 msgrprttsf aesckpvqqp safgsmkvsr dkdgskvttv vatpgggpdr pqevsytdtk  
61 vigngsfgvv yqaklcsgsge lvaikkvlqd krfknrelqi mrkldhcniv rlryffyssg  
121 ekkdevylnl vldyvpetvy rvarhysrak qtlpvyyvki ymyqlfrsla yihsfgichr  
181 dikpqnllld pdtavlklcd fgsakqlvrg epnvsyicsr yyrapelifg atdytssidv  
241 wsagcvlael llgqplfpgd sgvdqlveii kvlgtptreq iremnnpnyte fkfpqikahp  
301 wtkvfrprtp peialcsrl leytptarlt pleacahsf delrdpnvkl pngrdtpalf  
361 nfttqelssn pplatilipp hariqaaast ptnataasda ntgdrgqtnn aasasasnst

**FIG. 32**

**Human Glycogen synthase kinase-3 alpha (GSK-3 alpha).**

1 msgggpsggg pggsgrarts sfaepggggg gggggpggsa sgpggtgggk asvgamggv  
61 gasssgggpg gsggggsggg gagtsfpppg vklgrdsgkv ttvvatlgqq persqevayt  
121 dikvigngsf gvvyqarlae trelvaikkv lqdkrfknre lqimrkldhc nivrlryffy  
181 ssgekkdely lnlvleyvpe tvyrvahrft kakltipily vkvymyqlfr slayihsqgv  
241 chrdikpqnl lvdpdtavlk lcdfgsakql vrgepnvsyi csryyrapel ifgatdytss  
301 idvwsagcvl aelllgqpif pgdsgvdqlv eiikvlgtpt reqiremnpn ytefkfpqik  
361 ahpwtkvfk srtpeaialc ss1leytpss rlspleacah sffdclrc1g tqlpnrrplp  
421 plfnfsagel siqpsinail ipphlrspag tttltpssqa ltetptssdw qstdatptlt  
481 nss

**FIG. 33**

## Mouse Glycogen synthase kinase-3 beta.

1 msgrprttsf aesckpvqqp safgsmkvsr dkdgskvttv vatpgggpdr pqevsytdtk  
61 vigngsfgvv yqaklc当地 lvaikkvlqd krfknrelqi mrkldhcniv rlryffyssg  
121 ekkdevylnl vldyvpetvy rvarhysrak qtlpviyvkl ymyqlfrsla yihsfgichr  
181 dikpqnlld pdtavlklcd fgsakqlvrg epnvsyicsr yyrapelifg atdytssidv  
241 wsagcvlael llgqplifpgd sgvdqlveii kvlgtptreq iremnnpnyte fkfpqikahp  
301 wtkvfrprtp peaialcsrl leypttarlt pleacahsff delrdpnvkl pngrdtpalf  
361 nfttqelssn pplatilipp hariqaaaasp panataasdt nagdrgqtnn aasasasnst

**FIG. 34**

Mouse Glycogen synthase kinase-3 alpha (GSK-3 alpha).

1 masttamdvl eelssdssek qrsvnildsf vkmferias easflarqar nstinsreiq  
61 tairlllpge lcrrgtgcgk asvwamggg gassgvggg sggpgstsfl qpgvklghds  
121 rkvtvvvatv qqdpersqev actdikvign gsfgvvyqew ladtrelvai kkvlqdkrfk  
181 yrelqimckl dhcnivrlqy ffyssgekkd dlylnlvley vpetvyxvar hftkakliip  
241 iiyvkvymyq lfrslayihs qgvchrdinl lvdptailk lcdfgsakql vlgttvapel  
301 ytssidvxsa gcvlaellls qpiifpgdngv dqlveiikvl gptreqire mmpkytefkf  
361 pqikahpwtk vfksrtaprp lhsalacwst hhtqgsphlr lvptaslmnc gvsgpapqrp  
421 ptspcstsvl vicpsnhlsm pfssllt

**FIG. 35**

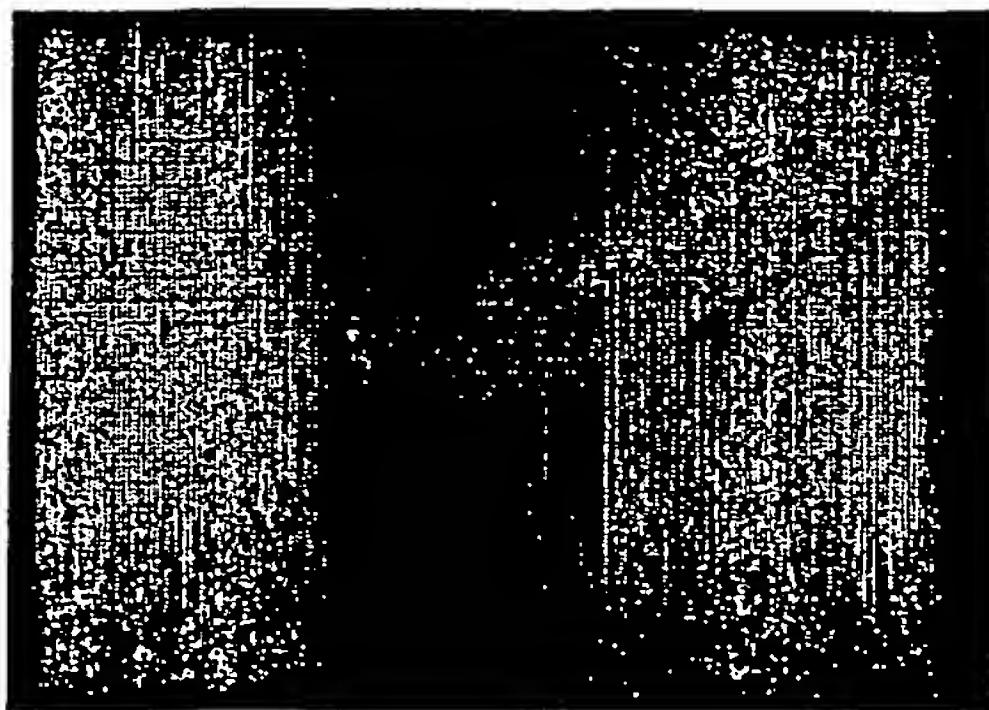
GSK-3 [*Caenorhabditis elegans*].

1 mnkql1scsl ksgkqvtmvv asvatdgvdq qveisyydqk vigngsfgvv flaklsttne  
61 mvaikkvlqd krfknrelqi mrklnhpniv klkyffyssg ekkdelylnl ileyvpetvy  
121 rvarhyskqr qqipmiyvkl ymyqlrlsla yihsigichr dikpqnlid pesgvklcd  
181 fgsakylvrr epnvsyicsr yyrapelifg atnytnsidv wsagtvmael llgqplifpgd  
241 sgvdqlveii kvlgtptreq iqsmnnpnyke fkfpqikahp wnkvfrvhtp aeaidliski  
301 ieytptsrpt pqaacqhaff delrnpdarl psgrpltle mdgpmgtgei sptsgdvagg  
361 sa

**FIG. 36**

***sgg-1* (GSK-3) inhibits constitutive **SKN-1** nuclear accumulation and induction of its target gene *gcs-1*.**

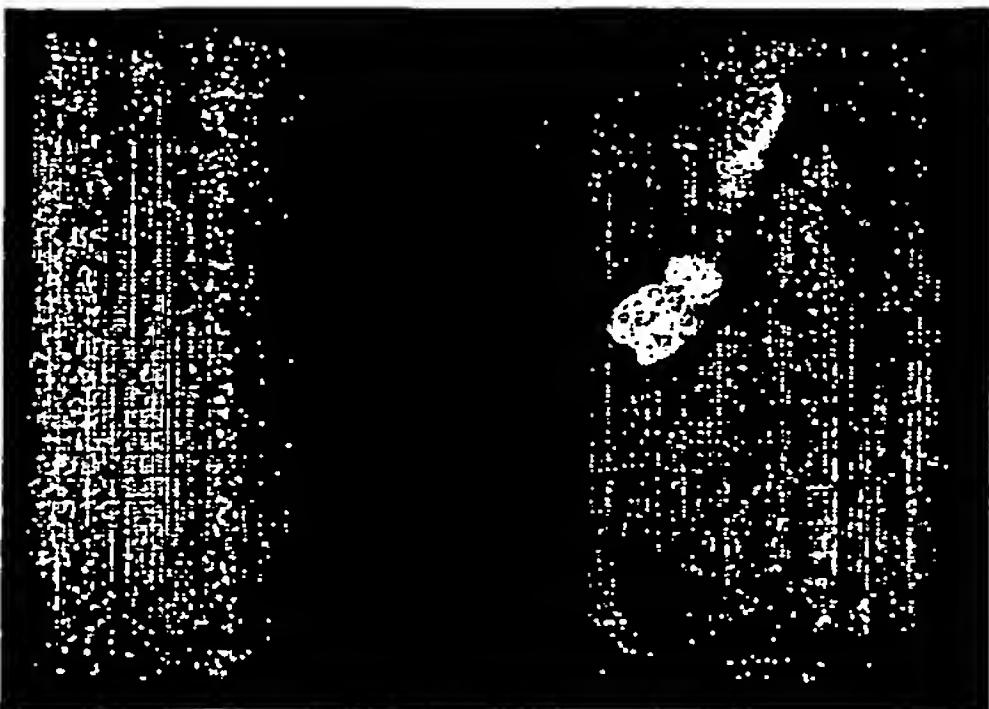
Control [*glo-1*(RNAi)]



*sgg-1*(RNAi)



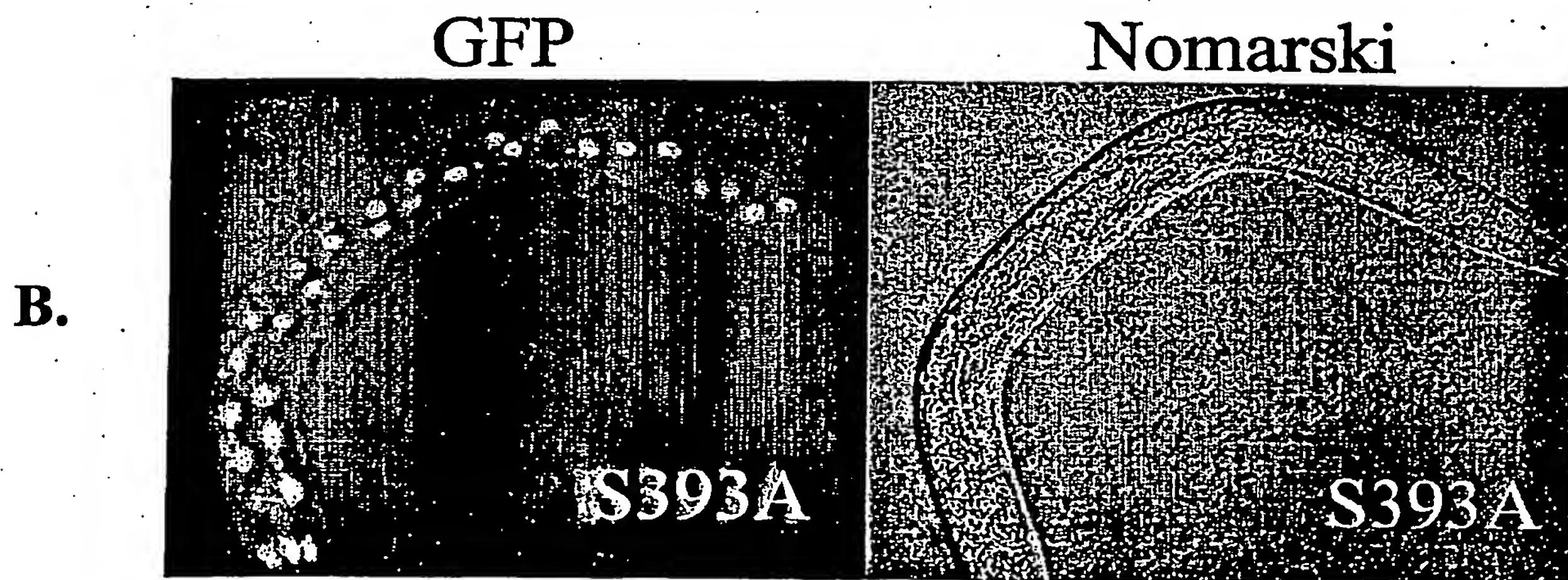
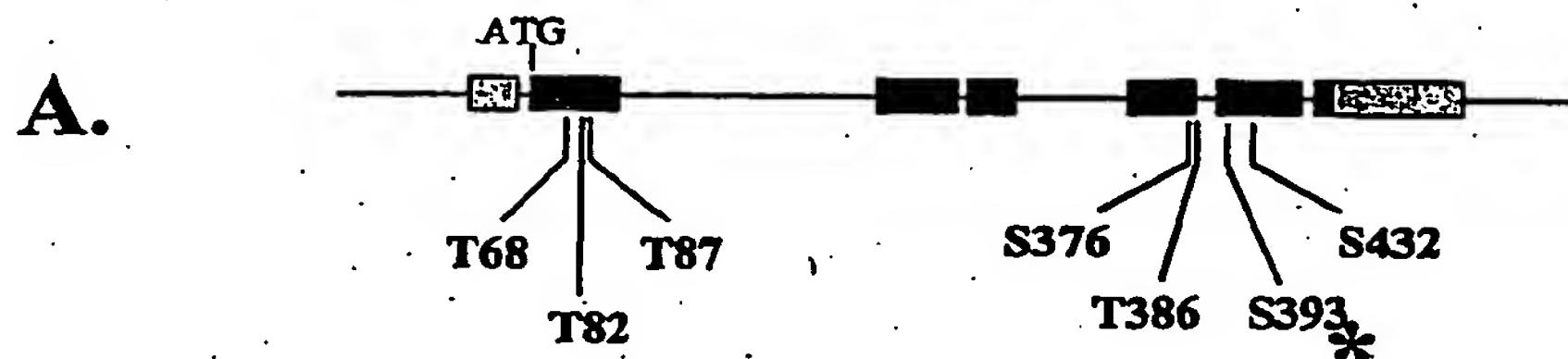
Control [*glo-1*(RNAi)]



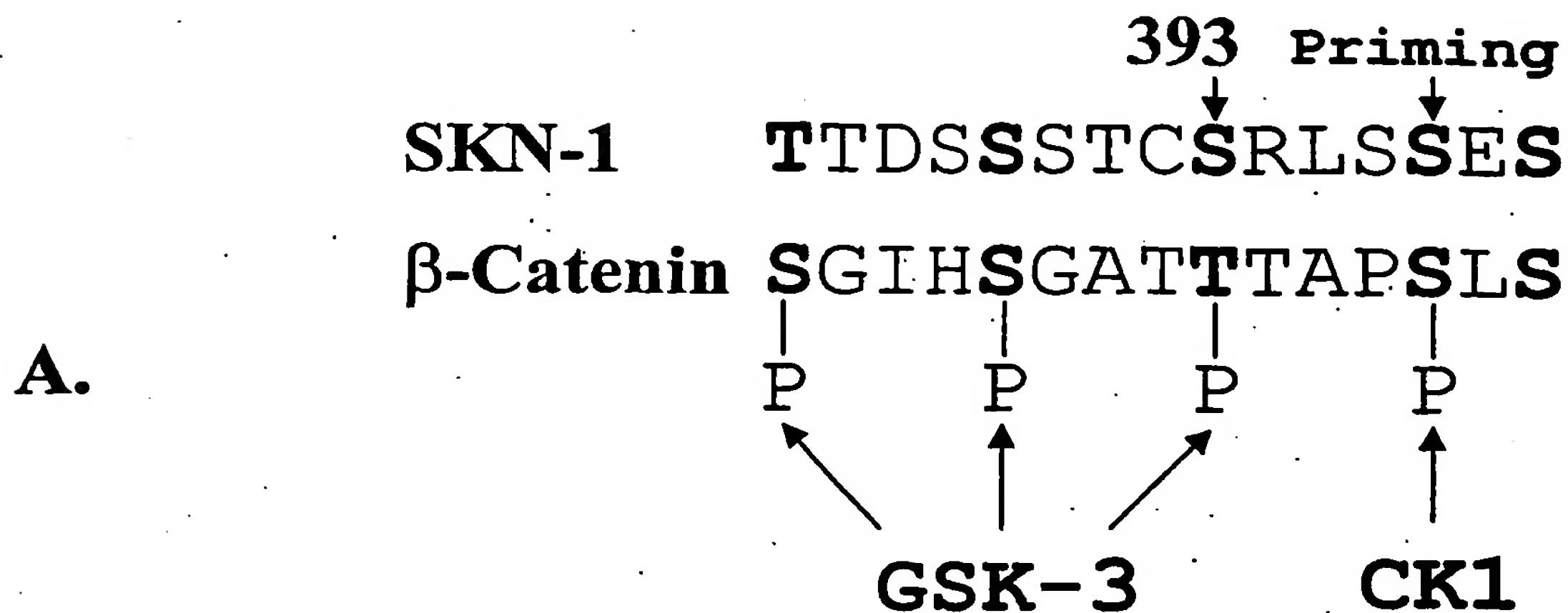
*sgg-1*(RNAi)



**Ala substitution at a predicted GSK-3 phosphorylation site results in nuclear localization of SKN-1**



**FIG. 38**

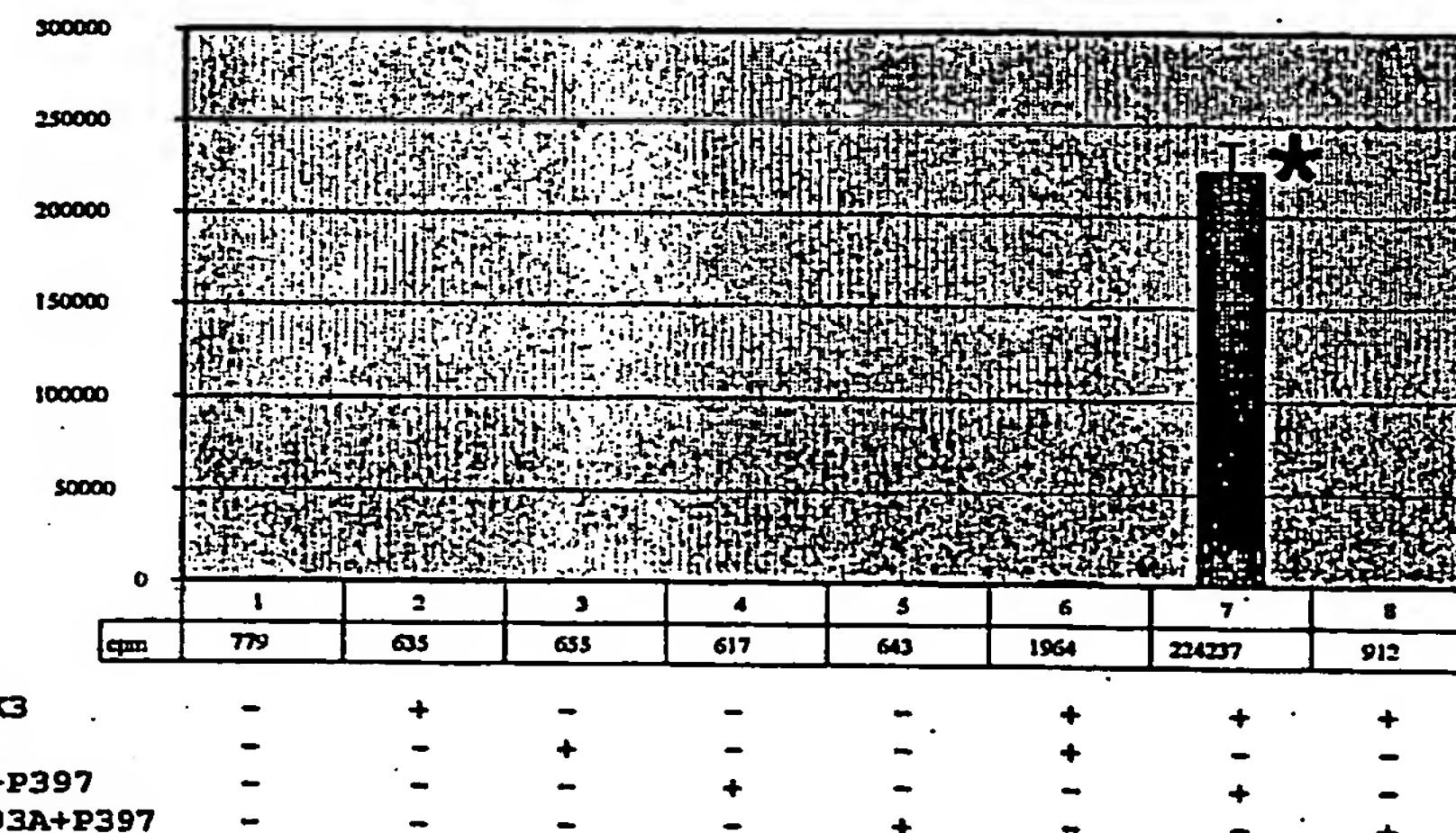


**Peptides:**

1. WT      DCTTDSSSTCSRLSSES<sup>393</sup>PRYTSE
2. WT+P397      DCTTDSSSTCSRLSSES<sup>397</sup>PRYTSE ★
3. S393A+P397      DCTTDSSSTCARLSSES<sup>393</sup>PRYTSE

**Assay:**

**B.**



**FIG. 39**